

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:56:54 ; Search time 79.2611 Seconds  
(without alignments)  
4199.299 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	5882	99.3	1178	3	AA71311	Aay71311 Human neu
2	5815	98.2	1192	4	AAU04591	Aau04591 Human Nog
3	5815	98.2	1192	5	ABP68600	Abp68600 Human pan
4	5815	98.2	1192	6	ABR59667	Abr59667 Human Nog
5	5810	98.1	1192	3	AA56967	Aay56967 Human MAG
6	5810	98.1	1192	4	AAB82349	Aab82349 Human NOG
7	5810	98.1	1192	5	ABG30938	Abg30938 Human Nog
8	5810	98.1	1192	5	ABB81078	Abb81078 Human neu
9	5526.5	93.3	1246	4	AAU33228	Aau33228 Novel hum

10	4560	77.0	983	6	ABU11573	Abu11573	Human MDD
11	4400	74.3	893	3	AAy95012	Aay95012	Human sec
12	4296.5	72.5	1163	3	AAy71310	Aay71310	Rat neuri
13	4296.5	72.5	1163	5	ABB81074	Abb81074	Rat neuro
14	4294.5	72.5	1162	3	AAy71557	Aay71557	Rat Nogo
15	4286.5	72.4	1163	3	AAy71384	Aay71384	Alternati
16	3388.5	57.2	974	3	AAy71560	Aay71560	Rat Nogo
17	3146.5	53.1	642	2	AAW58383	Aaw58383	Human sec
18	3146.5	53.1	642	4	AAB90682	Aab90682	Human BGl
19	2715	45.8	803	3	AAy71562	Aay71562	Rat Nogo
20	2529.5	42.7	737	3	AAy71386	Aay71386	Rat Nogo
21	2487.5	42.0	746	3	AAy71391	Aay71391	Rat Nogo
22	2457	41.5	736	3	AAy71398	Aay71398	Rat Nogo
23	2449.5	41.4	732	3	AAy71399	Aay71399	Rat Nogo
24	2405.5	40.6	695	3	AAy71387	Aay71387	Rat Nogo
25	2344.5	39.6	684	3	AAy71394	Aay71394	Rat Nogo
26	1948.5	32.9	552	3	AAy71388	Aay71388	Rat Nogo
27	1743	29.4	502	3	AAy71396	Aay71396	Rat Nogo
28	1634.5	27.6	475	3	AAy71389	Aay71389	Rat Nogo
29	1566.5	26.4	403	3	AAy71563	Aay71563	Rat Nogo
30	1552.5	26.2	457	3	AAy71392	Aay71392	Rat Nogo
31	1495.5	25.2	373	3	AAy53624	Aay53624	A bone ma
32	1495.5	25.2	373	3	AAy56969	Aay56969	Human MAG
33	1495.5	25.2	373	3	AAB24242	Aab24242	Human Nog
34	1495.5	25.2	373	4	AAB82350	Aab82350	Human NOG
35	1495.5	25.2	373	5	AAM47954	Aam47954	Human RTN
36	1495.5	25.2	373	5	ABP68601	Abp68601	Human pan
37	1495.5	25.2	373	5	ABB81079	Abb81079	Human neu
38	1487.5	25.1	373	5	ABG30937	Abg30937	Human Nog
39	1412	23.8	289	3	AAy56968	Aay56968	Human MAG
40	1327	22.4	284	3	AAy95030	Aay95030	Human clo
41	1264	21.3	356	3	AAy71390	Aay71390	Rat Nogo
42	1225.5	20.7	379	7	ADB85283	Adb85283	Rat fooce
43	1205.5	20.4	374	3	AAy71397	Aay71397	Rat Nogo
44	1196.5	20.2	361	3	AAy71385	Aay71385	Alternati
45	1189	20.1	359	3	AAy71558	Aay71558	Rat Nogo

# ALIGNMENTS

## RESULT 1

AAy71311

ID AAY71311 standard; protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 187  
 FT /label= Unknown  
 FT Misc-difference 188  
 FT /label= Unknown  
 FT Misc-difference 189  
 FT /label= Unknown  
 FT Misc-difference 190  
 FT /label= Unknown  
 FT Misc-difference 221  
 FT /label= Unknown  
 FT Misc-difference 328  
 FT /label= Unknown  
 FT Misc-difference 477  
 FT /label= Unknown  
 FT Region 977. .1012  
 FT /note= "Region specifically described in claim 16"  
 FT Region 994. .1174  
 FT /note= "Region specifically described in claim 16"  
 FT Region 1079. .1114  
 FT /note= "Region specifically described in claim 16"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Claim 11; Fig 13; 122pp; English.  
 XX  
 CC The present sequence is a human Nogo protein which is a potent neural  
 CC cell growth inhibitor and is free of all central nervous system (CNS)  
 CC myelin material with which it is natively associated. The human Nogo  
 CC sequence was derived by aligning human expressed sequence tags (ESTs)  
 CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525  
 CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments  
 CC displaying neurite growth inhibitory activity are used in the treatment  
 CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
 CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
 CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,  
 CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.

CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However the specification does not include sequences for  
CC these SEQ ID numbers

XX

SQ Sequence 1178 AA;

Query Match 99.3%; Score 5882; DB 3; Length 1178;  
Best Local Similarity 99.7%; Pred. No. 5.4e-296;  
Matches 1175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Db	1	MEDLDQSPLVSSSDSVPRPQPAFKYQFVREPED	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSS	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSS	120
Qy	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Db	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN	240
Db	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN	240
Qy	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV	300
Db	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV	300
Qy	301	IVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV	360
Db	301	IVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV	360
Qy	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH	420
Db	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH	420
Qy	421	EKDSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE	480
Db	421	EKDSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE	480
Qy	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL	540
Db	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL	540
Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600



Db	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSIGKE	660
Db	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSIGKE	660
Qy	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Qy	721	EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Db	721	EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Db	781	GKPYLESFKLSLVNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Qy	841	TETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	841	TETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLE	960
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	1021	SIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178

RESULT 2

AAU04591

ID AAU04591 standard; protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;  
KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
KW Krabbe's disease.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	1054. .1119
FT		/label= Lumenal_extracellular_domain
FT		/note= "This sequence is specifically claimed"
FT	Peptide	1055. .1094
FT		/label= Pep1
FT		/note= "Receptor binding inhibitory peptide. This
FT		sequence is specifically claimed"
FT	Peptide	1064. .1088
FT		/label= Pep2
FT		/note= "Receptor binding inhibitory peptide. This
FT		sequence is specifically claimed"
FT	Peptide	1074. .1098
FT		/label= Pep3
FT		/note= "Receptor binding inhibitory peptide. This
FT		sequence is specifically claimed"
FT	Peptide	1084. .1108
FT		/label= Pep4
FT		/note= "Receptor binding inhibitory peptide. This
FT		sequence is specifically claimed"
FT	Peptide	1095. .1119
FT		/label= Pep5
FT		/note= "Receptor binding inhibitory peptide. This
FT		sequence is specifically claimed"

XX

PN WO200151520-A2.

XX

PD 19-JUL-2001.

XX

PF 12-JAN-2001; 2001WO-US001041.

XX

PR 12-JAN-2000; 2000US-0175707P.

PR 26-MAY-2000; 2000US-0207366P.

PR 29-SEP-2000; 2000US-0236378P.

XX

PA (UYYA ) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2001-442138/47.

DR N-PSDB; AAS09453.

XX

PT Novel Nogo receptor protein useful for identifying modulator of Nogo  
PT protein or Nogo receptor protein, which is useful for treating central  
PT nervous system disorders.

XX

PS Example 1; Page 101-104; 109pp; English.

XX

CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon



Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSLKAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSLKAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAELGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 3

ABP68600

ID ABP68600 standard; protein; 1192 AA.

XX

AC ABP68600;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed protein SEQ ID NO 71.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
cytostatic; tumour.

XX

OS Homo sapiens.

XX



Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSPPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSPPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSF SKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSF SKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPPDV SALGH	945

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          |||
Db      901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAALA- 959
Qy      946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
          |||
Db      960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSALSKTSVVDLLYWRDIKKTGV 1019
Qy      1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES 1065
          |||
Db      1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES 1079
Qy      1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
          |||
Db      1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
Qy      1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||
Db      1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

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RESULT 4

ABR59667

ID ABR59667 standard; protein; 1192 AA.

XX

AC ABR59667;

XX

DT 22-JUL-2003 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;  
KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

XX

OS Homo sapiens.

XX

PN WO2003031462-A2.

XX

PD 17-APR-2003.

XX

PF 04-OCT-2002; 2002WO-US032007.

XX

PR 06-OCT-2001; 2001US-00972599.

XX

PA (UYYA ) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2003-393433/37.

DR

N-PSDB; ACC81048.

XX

PT New human Nogo receptor polypeptides and nucleic acids, useful for  
PT decreasing inhibition of axonal growth by a central nervous system  
PT neuron, or in treating central nervous system disease, disorder or  
PT injury, e.g. spinal cord injury.





Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESTTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESTTETSFESMI	780
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSALSSTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 5

AA56967

ID AAY56967 standard; protein; 1192 AA.

XX

AC AAY56967;

XX  
DT 25-APR-2000 (first entry)  
XX  
DE Human MAGI polypeptide.  
XX  
KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
KW psychiatric disorder; developmental disorder; inflammatory disorder;  
KW stroke; cytostatic; cerebroprotective; neuroprotective.  
XX  
OS Homo sapiens.  
XX  
PN WO200005364-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 21-JUL-1999; 99WO-GB002360.  
XX  
PR 22-JUL-1998; 98GB-00016024.  
PR 19-JUL-1999; 99GB-00016898.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Michalovich D, Prinjha RK;  
XX  
DR WPI; 2000-182693/16.  
DR N-PSDB; AAZ56886.  
XX  
PT Novel polypeptides related to neuroendocrine-specific proteins and  
PT polynucleotides useful for diagnosis of various diseases and for  
PT treatment of cancer and neurological disorders.  
XX  
PS Claim 2; Page 20-21; 35pp; English.  
XX  
CC The invention relates to human MAGI protein, which is similar to  
CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
CC and antibodies are useful for treating diseases, including neuropathies,  
CC spinal injury, neuronal degeneration, neuromuscular disorders,  
CC psychiatric disorders and developmental disorders, cancer, stroke and  
CC inflammatory disorders. The polynucleoitde is also useful for chromosome  
CC localization and for tissue expression studies. The present sequence  
CC represents the human MAGI protein  
XX  
SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 3; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120

Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:   :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKAEQIRETETFSDSPIEIIIDFPTLISSKTDSESKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKAEQIRETETFSDSPIEIIIDFPTLISSKTDSESKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSALA-	959



CC The present sequence is that of human NOGO-A. NOGO-A is a previously  
 CC known splice variant of the human NOGO gene on chromosome 2p21. The  
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It  
 CC provides NOGO-C polypeptides and polynucleotides, and methods for  
 CC producing such polypeptides by recombinant techniques. Also disclosed are  
 CC methods for utilising NOGO-C polypeptides and polynucleotides in the  
 CC treatment of diseases including neuropathies, spinal injury, brain  
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease  
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders  
 CC and developmental disorders. Also provided are methods for identifying  
 CC agonists and agonists for use in treating conditions associated with NOGO  
 CC -C imbalance, and diagnostic assays for detecting diseases associated  
 CC with inappropriate NOGO-C activity or levels

XX

SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 4; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP	120
Qy	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Db	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:   :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLDGPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586

Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPVDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPVDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAIGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAIGH	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAELGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELGKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 7

ABG30938

ID ABG30938 standard; protein; 1192 AA.

XX

AC ABG30938;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;

KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;

KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;

KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;  
 KW Nogo-associated disease; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257483-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 18-JAN-2002; 2002WO-GB000228.  
 XX  
 PR 18-JAN-2001; 2001GB-00001312.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
 XX  
 DR WPI; 2002-599722/64.  
 DR N-PSDB; ABK90134.  
 XX  
 PT Identifying modulators of Nogo or BACE activity for treating acute  
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
 PT providing and monitoring interaction between Nogo and BACE polypeptides.  
 XX  
 PS Disclosure; Page 59-62; 68pp; English.  
 XX  
 CC The present invention relates to a new method of identifying modulators  
 CC of Nogo function or BACE activity. The method involves providing Nogo and  
 CC BACE polypeptides capable of binding with each other, monitoring the  
 CC interaction between these polypeptides, and determining if the test agent  
 CC is a modulator of Nogo or BACE activity. The method is useful in treating  
 CC acute neuronal injuries, such as spinal or head injury, stroke,  
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
 CC hypertrophy) of the central nervous system. The BACE polypeptide is  
 CC useful in screening methods to identify agents that may act as modulators  
 CC of BACE activity and in particular agents that may be useful in treating  
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
 CC and the polynucleotide encoding the BACE polypeptide are useful in  
 CC manufacturing a medicament for the treatment or prevention of disorders  
 CC responsive to the modulation of Nogo activity, in alleviating the  
 CC symptoms or improving the condition of a patient suffering from this  
 CC disorder, in axon regeneration, or in preventing metastasis or spreading  
 CC of a cancer. The polynucleotide may also be an essential component in  
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
 CC techniques. The present amino acid sequence represents the human NogoA  
 CC protein of the invention  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 5; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:   :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDSIPDVPQKQDETVMVLVKESLTETS FESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDSIPDVPQKQDETVMVLVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885





PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR N-PSDB; ABN86601.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 PS Example; Page 53-56; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the human  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 5; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60  
  
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120  
  
 Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	: : :     SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKGSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005
		TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	

Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019  
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLES 1065  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLES 1079  
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 9

AAU33228

ID AAU33228 standard; protein; 1246 AA.

XX

AC AAU33228;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #3719.

XX

KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US008656.

XX

PR 18-APR-2000; 2000US-00552929.

PR 26-JAN-2001; 2001US-00770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy.

XX

PS Claim 20; Page 737; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent



Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646  
 |||  
 Db 642 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 701  
 |||  
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705  
 |||  
 Db 702 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 761  
 |||  
 Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI 765  
 |||  
 Db 762 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI 821  
 |||  
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 |||  
 Db 822 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 881  
 |||  
 Qy 826 SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 |||  
 Db 882 SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 941  
 |||  
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH 945  
 |||  
 Db 942 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA- 1000  
 |||  
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV 1005  
 ||| : |||  
 Db 1001 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1060  
 ||| : |||  
 Qy 1006 VFGAS-LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY-- 1062  
 ||| : |||  
 Db 1061 VFGASAVFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAISG 1120  
 ||| : |||  
 Qy 1063 -LESEVAISEELVQKYSNSALGHV-NCTIKELRR---LFLVDDLVDLSLK-FAVLMWVFTY 1116  
 ||| : : | : ||| : ||| : | | | : |||  
 Db 1121 NLESCLYLRELGSGRYSNSALGSMWNCTVKGNFRAPSFFSWMDLVDLSLRSFAVLMWVFTY 1180  
 ||| : : | : ||| : ||| : | | | : |||  
 Qy 1117 VGALFNGLTLL-----ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 1170  
 || | || : | || : |||  
 Db 1181 VGCL--GLMVLDTTGFWALNFISSSGSWLIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 1238  
 |||  
 Qy 1171 PGLKRKAE 1178  
 |||  
 Db 1239 PGLKRKAE 1246  
 |||

RESULT 10

ABU11573

ID ABU11573 standard; protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;

KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
KW gene therapy; protein replacement therapy; cell proliferative disorder;  
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
KW psoriasis; hepatitis.

XX  
OS Homo sapiens.

XX  
PN WO200279449-A2.

XX  
PD 10-OCT-2002.

XX  
PF 27-MAR-2002; 2002WO-US009944.

XX  
PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX  
PA (INCY-) INCYTE GENOMICS INC.

XX  
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX  
DR WPI; 2003-058431/05.

DR N-PSDB; ABX34563.

XX  
PT New purified disease detection and treatment molecule proteins and  
PT polynucleotides, useful for diagnosing, treating or preventing cancers  
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
PT or hepatitis.

XX  
PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.

XX  
CC This invention describes a novel disease detection and treatment molecule  
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
CC and the polypeptides of the invention can be used for gene therapy,  
CC protein replacement therapy and are useful for treating a variety of  
CC diseases or conditions. These polypeptides or polynucleotides are  
CC particularly useful for diagnosing, treating or preventing cell  
CC proliferative disorders (e.g. cancers including adenocarcinoma,  
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded

CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 983 AA;

Query Match 77.0%; Score 4560; DB 6; Length 983;  
Best Local Similarity 97.1%; Pred. No. 1.2e-227;  
Matches 919; Conservative 8; Mismatches 11; Indels 8; Gaps 3;

```
Qy      240 NLSTVL-----PTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVS 293
          |::|::| : : ::|||
Db      39 NMNTLVICQQYYPLKEHFKNVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVS 98

Qy      294 PKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKD 353
          |||
Db      99 PKAESAVIVANPREEIIVKNKDEEEKLVSNILHNNQQELPTALTKLVKEDEVVSSEKAKD 158

Qy      354 SFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFAD 413
          |||
Db      159 SFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFAD 218

Qy      414 SLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPT 473
          |||
Db      219 SLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDP 278

Qy      474 SENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMP 533
          |||
Db      279 SENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMP 338

Qy      534 EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATP 593
          |||
Db      339 EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATP 398

Qy      594 SPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL 653
          |||
Db      399 SPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL 458

Qy      654 -KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP 712
          |||
Db      459 KKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP 518

Qy      713 VPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEK 772
          |||
Db      519 VPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEK 578

Qy      773 LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI 832
          |||
Db      579 LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI 638

Qy      833 SKEAQIRETETFSDDSSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA 892
          |||
Db      639 SKEAQIRETETFSDDSSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA 698

Qy      893 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAEIES 952
          |||
```



Db 699 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALA-TQAEIES 757

Qy 953 IVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLF 1012  
 ||||| : |||||

Db 758 IVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLF 817

Qy 1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 1072  
 |||||

Db 818 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 877

Qy 1073 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 1132  
 |||||

Db 878 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 937

Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||

Db 938 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 983

RESULT 11

AA95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22\_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;  
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
 KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

\*PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX

PF 24-AUG-1999; 99WO-US019351.

XX

PR 24-AUG-1998; 98US-0097638P.

PR 24-AUG-1998; 98US-0097659P.

PR 09-SEP-1998; 98US-0099618P.

PR 28-SEP-1998; 98US-0102092P.

PR 25-NOV-1998; 98US-0109978P.

PR 23-DEC-1998; 98US-0113645P.

PR 23-DEC-1998; 98US-0113646P.

PR 23-AUG-1999; 99US-00379246.

XX

PA (ALPH-) ALPHAGENE INC.

XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

XX

PT New secreted or transmembrane proteins and polynucleotides encoding them,  
PT useful for treating neurodegenerative disorders, autoimmune diseases and  
PT cancer.

XX

PS Claim 73; Page 322-325; 357pp; English.

XX

CC The invention relates to 40 human secreted proteins (AA94981-Y95020),  
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins  
CC of the invention include those that are thought to be only partially  
CC secreted, i.e., transmembrane proteins. The proteins of the invention may  
CC exhibit one or more activities selected from the following: cytokine  
CC activity; cell proliferation; differentiation; immune modulation;  
CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
CC proteins may be administered to patients as vaccines, and the nucleotides  
CC may be used as part of a gene therapy regime. Diseases or conditions that  
CC may be treated using the proteins or nucleotides of the invention include  
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
CC allergic reactions such as asthma and anaemia. They may also be used for  
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
CC activity may additionally be useful as contraceptives. Nucleic acid  
CC sequences of the invention may be used in chromosome mapping, and as a  
CC source of diagnostic primers and probes. The present sequence represents  
CC one of the 40 proteins of the invention

XX

SQ Sequence 893 AA;

Query Match 74.3%; Score 4400; DB 3; Length 893;  
Best Local Similarity 98.9%; Pred. No. 2e-219;  
Matches 884; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

Qy	286	MGSSFSVSPKAESAVIVANPREEIIVKNKDDEEEKLVSNILHXQQELPTALTCLKVKEDEV	345
Db	1	MGSSFSVSPKAESAVIVANPREEIIVKNKDDEEEKLVSNILHNQQELPTALTCLKVKEDEV	60
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESK	405
Db	61	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESK	120
Qy	406	VDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNI	465
Db	121	VDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNI	180
Qy	466	FPLLEDPTSENXTDEKKIEEKKQAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVT	525
Db	181	FPLLDGPTSENKTDEKKIEEKKQAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVT	240
Qy	526	EEVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS	585
Db	241	EEVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS	300

Qy 586 FEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY 645  
 |||||  
 Db 301 FEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY 360  
 |||||  
 Qy 646 EEAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYS 704  
 |||||  
 Db 361 EEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYS 420  
 |||||  
 Qy 705 EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESM 764  
 |||||  
 Db 421 EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESM 480  
 |||||  
 Qy 765 IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV 824  
 |||||  
 Db 481 IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV 540  
 |||||  
 Qy 825 YSNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTD SFSKLAREYTDLEVSHKSE 884  
 |||||  
 Db 541 YSNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTD SFSKLAREYTDLEVSHKSE 600  
 |||||  
 Qy 885 IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS SKVLLLPPDV SALG 944  
 |||||  
 Db 601 IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS SKVLLLPPDV SALA 660  
 |||||  
 Qy 945 HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDI LYWRDIKKTG 1004  
 ||||| : |||||  
 Db 661 -TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIF SAE LSKTSVVDI LYWRDIKKTG 719  
 |||||  
 Qy 1005 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLE 1064  
 |||||  
 Db 720 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLE 779  
 |||||  
 Qy 1065 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGL 1124  
 |||||  
 Db 780 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGL 839  
 |||||  
 Qy 1125 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKIPGLKRKAE 1178  
 |||||  
 Db 840 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKIPGLKRKAE 893  
 |||||

100%  
 990-178

RESULT 12

AA71310

ID AAY71310 standard; protein; 1163 AA.

XX

AC AAY71310;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.

XX

OS Rattus sp.

XX

Key	Location/Qualifiers
FT Inhibitory-site	1. .171
FT	/note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site	30
FT	/note= "Casein kinase II site"
FT Region	31. .58
FT	/note= "Acidic region"
FT Region	31. .57
FT	/note= "Region specifically described in claim 16"
FT Region	172. .259
FT	/note= "This region is not essential for inhibitory activity"
FT Modified-site	233
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	242. .244
FT	/note= "Asn is N-glycosylated"
FT Modified-site	291
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	295
FT	/note= "Protein kinase C (PKC) site"
FT Misc-difference	404
FT	/note= "Encoded by TTG"
FT Modified-site	436
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	468. .470
FT	/note= "Asn is N-glycosylated"
FT Modified-site	484
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	488
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	502
FT	/note= "Casein kinase II site"
FT Inhibitory-site	542. .722
FT Modified-site	576
FT	/note= "Casein kinase II site"
FT Peptide	623. .640
FT	/note= "used as immunogen to generate antibody AS 472"
FT Modified-site	626
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	694. .696
FT	/note= "Asn is N-glycosylated"
FT Modified-site	715
FT	/note= "Casein kinase II site"
FT Peptide	762. .1163
FT	/note= "used as immunogen to generate antibody AS Bruna"
FT Modified-site	784
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	821
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	850
FT	/note= "Protein kinase C (PKC) site"
FT Modified-site	855
FT	/note= "Protein kinase C (PKC) site"

FT Modified-site 863  
 FT /note= "Casein kinase II site"  
 FT Modified-site 868  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 893  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 912. .914  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 925. .927  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 954  
 FT /note= "PKC and casein kinase II sites"  
 FT Modified-site 956  
 FT /note= "PKC and casein kinase II sites"  
 FT Region 975. .1162  
 FT /note= "This region is not essential for inhibitory  
 FT activity"  
 FT Region 976. .1163  
 FT /note= "C-terminal common region found in Nogo A, B and C  
 FT isoforms"  
 FT Domain 988. .1023  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region specifically  
 FT described in claim 16"  
 FT Modified-site 1024  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1071. .1073  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 1073  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1089  
 FT /note= "Protein kinase C (PKC) site"  
 FT Domain 1090. .1125  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region specifically  
 FT described in claim 16"  
 FT Modified-site 1141. .1143  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 1143  
 FT /note= "Protein kinase C (PKC) site"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 DR N-PSDB; AAD01173.  
 XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 3; Fig 2A; 122pp; English.

XX

CC The present sequence is a rat Nogo A protein which is a potent neural  
CC cell growth inhibitor and is free of all central nervous system (CNS)  
CC myelin material with which it is natively associated. The protein was  
CC derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated  
CC from hexanucleotides-primed rat brain stem/spinal cord library, and Olil8  
CC cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins  
CC and fragments displaying neurite growth inhibitory activity are used in  
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,  
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: The present sequence  
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown  
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence  
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However, the specification does not include sequences for  
CC these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 3; Length 1163;  
Best Local Similarity 74.0%; Pred. No. 6.2e-214;  
Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58  
| | | : | | | | | | | | | | | | | | | | | | : | | : | | | | | | | | |  
Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK 60

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118  
| | | | | | | | | | | | | | | | | | | | | | | | : | | : |  
Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKR 178  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224  
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 167 RGSGSVDETLFALPAASEVPVPSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284  
| | | | | | | | | | | | : | | : | : | | | | : | | : | | | | | | | | |

Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIVKNKDDEEKLVSNNILHXQQELPTALTCLVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSGRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK	523
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVLAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVGSIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPVDPHSELVEDSSPDSEPVDLFSDDSIQVDPQKQDETVMLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIQVDPQQTQEEAVMLMKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESETFSDDSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVS	942
Db	871	SEIANIQSGADSLPCLLEPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFN	1107

QY 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||:|||||:|||||:|||||:  
 Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 13

ABB81074

ID ABB81074 standard; protein; 1163 AA.

XX

AC ABB81074;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA ) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.

XX

PS Example 5; Page 44-47; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and



CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 5; Length 1163;  
 Best Local Similarity 74.0%; Pred. No. 6.2e-214;  
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy 1 MEDLDQSPVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58  
 |||:||||| ||||| ||||| ||||| ||||| |||||:||||| |||||  
 Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK 60

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118  
 ||||| || ||| |||:|| :| ||||| ||||| |||||: || : |  
 Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178  
 ||| |||| ||||| ||||| ||||| || || ||||| |||||  
 Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224  
 ||| : |||| |||||:|:||||| ||||| |||  
 Db 167 RSGSVDETFLFALPAASEPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284  
 |||| ||||| ||||| | :|||:| :|||:| :| :||| |||||  
 Db 227 SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPVNRDLAEFSELEYS 286

Qy 285 EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDE 344  
 ||||| ||| |||:| | :||:|:|:|:| : || : || || ||  
 Db 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG----KEDR 340

Qy 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403  
 ||| || | ||| :|| ||:|||||||: ||||: | | |:| | :|||  
 Db 341 VVSPEKTMDIFNEMQMSVAVPREEYADFKPFEQAWVKDITYEGSRDVLAA----RANVE 396



XX  
 AC AAY71557;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is  
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-  
 CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were



Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSIGIKEEIKPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESETFSDDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLNPKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSVA	942
Db	871	SEIANIQSGADSLPCLELPCDLNPKNIYPK--DEVHVSDEFSENRRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFN	1107
Qy	1123	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKA	1177
Db	1108	GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKA	1162

RESULT 15

AAAY71384

ID AAY71384 standard; protein; 1163 AA.

XX

AC AAY71384;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening.

```

XX
OS   Rattus sp.
XX
FH   Key          Location/Qualifiers
FT   Inhibitory-site 1. .171
FT                               /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                               /note= "Casein kinase II site"
FT   Region          31. .58
FT                               /note= "Acidic region"
FT   Region          172. .259
FT                               /note= "This region is not essential for inhibitory
FT                               activity"
FT   Misc-difference 223
FT                               /label= Unknown
FT                               /note= "There is Leu at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   233
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   242. .244
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   291
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   295
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 404
FT                               /note= "There is Ile at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   436
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   468. .470
FT                               /note= "Asn is N-glycosylated"
FT   Misc-difference 469
FT                               /label= Unknown
FT                               /note= "There is Lys at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   484
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   488
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   502
FT                               /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                               /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                               /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 661
FT                               /note= "There is Asn at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   694. .696
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   715
FT                               /note= "Casein kinase II site"
FT   Peptide         762. .1163

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FT /note= "used as immunogen to generate antibody AS Bruna"  
 FT Modified-site 784  
 FT /note= "Protein kinase C (PKC) site"  
 FT Misc-difference 820  
 FT /note= "There is Leu at this position in the sequence  
 FT shown in AAY71310"  
 FT Modified-site 821  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 850  
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 FT /note= "C-terminal hydrophobic region"  
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 FT /note= "Protein kinase C (PKC) site"  
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 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 1073  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1089  
 FT /note= "Protein kinase C (PKC) site"  
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 FT /note= "C-terminal hydrophobic region"  
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 FT Modified-site 1143  
 FT /note= "Protein kinase C (PKC) site"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 3; Fig 13; 122pp; English.

XX

CC The present sequence is an alternative version of rat Nogo A protein  
CC which is a potent neural cell growth inhibitor and is free of all central  
CC nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. Note: The present  
CC sequence is an alternative version of the Nogo A sequence shown in Fig.  
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ  
CC ID NO: 29 in disclosure of the specification. However the specification  
CC does not include sequences for these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 72.4%; Score 4286.5; DB 3; Length 1163;  
Best Local Similarity 74.1%; Pred. No. 2.1e-213;  
Matches 886; Conservative 104; Mismatches 155; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58  
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Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSPVSTVP 118  
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Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKR 178  
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Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224  
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Db 167 RSGSGVDETLFALPAASEPVIIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSTL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284  
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Qy 285 EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDE 344  
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Db 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340

Qy 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERWVEVKDSKEDS-DMLAAGGKIESNLE 403  
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Qy 404 SKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463  
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Qy 464 NIFPLLEDPTSENXTDEKKIEEKKAIIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK 523  
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Job time : 85.2611 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:02:30 ; Search time 23.2562 Seconds  
(without alignments)  
2615.013 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

		%					
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No.	Score	Match	Length	DB	ID	Description	
1	931	15.7	199	2	US-08-700-607-1	Sequence 1, Appli	
2	787.5	13.3	776	2	US-08-700-607-5	Sequence 5, Appli	
3	705	11.9	356	2	US-08-700-607-6	Sequence 6, Appli	
4	688	11.6	208	2	US-08-700-607-7	Sequence 7, Appli	
5	671	11.3	267	2	US-08-700-607-8	Sequence 8, Appli	
6	541.5	9.1	168	4	US-09-149-476-563	Sequence 563, App	
7	513	8.7	241	2	US-08-700-607-3	Sequence 3, Appli	
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10	316	5.3	8991	4	US-08-714-741-32	Sequence 32, Appl	
11	296.5	5.0	2468	4	US-09-976-594-726	Sequence 726, App	

12	285	4.8	92	4	US-09-149-476-411	Sequence 411, App
13	276.5	4.7	1786	3	US-08-973-462-8	Sequence 8, Appli
14	267.5	4.5	1601	4	US-09-345-473E-40	Sequence 40, Appl
15	265	4.5	1596	4	US-08-978-277A-4	Sequence 4, Appli
16	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
17	256	4.3	1780	1	US-08-769-309A-5	Sequence 5, Appli
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19	238	4.0	1346	2	US-08-635-121-2	Sequence 2, Appli
20	238	4.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
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24	237.5	4.0	1313	4	US-07-757-022B-142	Sequence 142, App
25	237.5	4.0	1314	4	US-07-757-022B-50	Sequence 50, Appl
26	237.5	4.0	1320	4	US-07-757-022B-46	Sequence 46, Appl
27	237.5	4.0	1320	4	US-07-757-022B-60	Sequence 60, Appl
28	237.5	4.0	1354	4	US-07-757-022B-48	Sequence 48, Appl
29	237.5	4.0	1361	4	US-07-757-022B-40	Sequence 40, Appl
30	237.5	4.0	1363	4	US-07-757-022B-52	Sequence 52, Appl
31	237.5	4.0	1404	4	US-07-757-022B-2	Sequence 2, Appli
32	237.5	4.0	1404	4	US-07-757-022B-62	Sequence 62, Appl
33	234.5	4.0	941	4	US-07-757-022B-14	Sequence 14, Appl
34	234.5	4.0	1022	4	US-07-757-022B-84	Sequence 84, Appl
35	234.5	4.0	1038	4	US-07-757-022B-74	Sequence 74, Appl
36	234.5	4.0	1049	4	US-07-757-022B-58	Sequence 58, Appl
37	234.5	4.0	1140	4	US-07-757-022B-104	Sequence 104, App
38	233.5	3.9	1320	4	US-10-164-595-58	Sequence 58, Appl
39	233.5	3.9	1404	4	US-10-164-595-78	Sequence 78, Appl
40	233.5	3.9	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
41	228	3.8	977	4	US-09-010-147B-18	Sequence 18, Appl
42	226.5	3.8	630	3	US-08-973-462-9	Sequence 9, Appli
43	225.5	3.8	2954	4	US-09-150-867-1	Sequence 1, Appli
44	225	3.8	783	6	5231168-2	Patent No. 5231168
45	225	3.8	3256	4	US-09-919-172-98	Sequence 98, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

##### ; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304



```

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

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Best Local Similarity 31.9%; Pred. No. 3.6e-40;
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

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Qy      633 --ESIKHEPENPPPYEEA-----MSVSLKVSGIKEEIKEPENINAAL-----QET 675
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Qy      676 EAPYISIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722
      ||||  ||  :| |  ||: :  : : |: ::
Db      260 FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309

Qy      723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF 761
      |||: |  |  ||  | : |  || : :||:
Db      310 PSPDTPVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQKGKGSISEDELITAIKEA----- 363

Qy      762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821

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; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

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Query Match          11.9%; Score 705; DB 2; Length 356;
Best Local Similarity 42.6%; Pred. No. 1.4e-35;
Matches 168; Conservative 55; Mismatches 86; Indels 85; Gaps 11;

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Db      30 QYSILREEREAEELDSELI---IESCDASSASEESPKRE----QDSPPMK-----PSALDA 77

Qy      863 KTDSFSKLALEYTDLEVSHKSEIANAPDGAGSL---PCTELPHDLSLKNIQPKVEEKISF 919
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Db      78 -----IREETGVRAEERAPSRRGLAEPGSFLDYPSTE-----PQPGPE----- 115

Qy      920 SDDFSKNGSATS KVVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPTS 979
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Db      116 -----LPPGDGAL-----EPETPMLP-----RKPEEDSSSNQSPA 145

Qy      980 A-----IFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVS 1024
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Db      146 ATKGPGLPGPGAPPPLLF---LNKQKAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVVS 202

Qy      1025 VTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH 1084
      | | | : | | | | | | | | | | | | | | | | | | | | | :
Db      203 VVAYIALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFY 262

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Db      263 VNSTLKELRRLFLVQDLVDLSLKFVLMWLLTYVGALFNGLTLLLMAVVSMFTLPVVVYVKH 322

Qy      1145 QAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
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Db      323 QAQIDQYLGLVVRTHINAVVAKIQAKIPGAKRHAE 356

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RESULT 4
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708

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Qy 1168 AKIPGLKRKAE 1178  
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Db 198 AKIPGAKRHAE 208

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 281046  
US-08-700-607-8

Query Match 11.3%; Score 671; DB 2; Length 267;  
Best Local Similarity 66.3%; Pred. No. 1.1e-33;  
Matches 124; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

Qy 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 1047  
|: :|||||||:|:|:|: | || || |:|:|: ||:|:| | ||||| |:  
Db 9 KSQAIDLLYWRDIKQTGIVFGSFLLLLSLTVFSVSVVAYLALAALSATISFRIYKSVL 68



; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
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; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          9.1%; Score 541.5; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 5e-26;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

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Qy      1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFRAYLESEVAISEE 1072
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Db      1 MLLSLAAFSVISVSVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy      1073 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 1132
          | |:|  |:|  |:  :  ||||:|:|:|  ||  |:  ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGAVFNGITLLILAE 120

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Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178  
 :||||:||||: ||||:|:| | : ||||:|:| |:|  
 Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607  
 ; Patent No. 5858708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Goli, Surya K.  
 ; APPLICANT: Hillman, Jennifer L.  
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/700,607  
 ; FILING DATE: Filed Herewith  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0114 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 241 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: THP1NOB01  
 ; CLONE: 31870

US-08-700-607-3

Query Match 8.7%; Score 513; DB 2; Length 241;  
 Best Local Similarity 47.7%; Pred. No. 4.7e-24;  
 Matches 102; Conservative 37; Mismatches 55; Indels 20; Gaps 1;

Qy 263 AEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022  
 || | : : : ||: ||: ||| ||| :| :||| ||:

Db 20 AEPSAPGGGGSPGACPALGTKSCSSSCAVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSV 79

Qy 1023 VSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSAL 1082  
 :|| :|: |||||:||||| ||||:||||:||||: ||: :| | | :|:|

Db 80 ISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139

Qy 1083 GHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYE 1142  
 |:| :| : |||||:||||| || ||: ||||:||||:||||| : : |||:|

Db 140 VHINRAKLIIRLFLVEDLVDLSKLAVFMWLMTYVGAVFNGITLLILAELLIXSVPIVYX 199

Qy 1143 RHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRK 1176  
 :: | : | | : :|

Db 200 KY-----KVPSKTPWNRQK 213

RESULT 8

US-09-621-976-4600  
 ; Sequence 4600, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 4600  
 ; LENGTH: 75  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 58  
 ; OTHER INFORMATION: Xaa = His,Pro  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 28  
 ; OTHER INFORMATION: Xaa = Met,Val  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 19  
 ; OTHER INFORMATION: Xaa = Pro,Gln  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 53  
 ; OTHER INFORMATION: Xaa = Ser,Tyr  
 US-09-621-976-4600

Query Match 5.8%; Score 344.5; DB 4; Length 75;  
 Best Local Similarity 82.6%; Pred. No. 1.9e-14;  
 Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
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Db 1 MEDLDQSPLVSSSDSPPRXQPAFKYQFXREPEDEE-----EDLEELEVLERKPA 49

Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86



Db 50 AGLXAAPVXTAPAAGAPLMDEFGNDFV 75

## RESULT 9

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US-09-621-976-4601
; Sequence 4601, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4601
;   LENGTH: 75
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 58
;   OTHER INFORMATION: Xaa = His,Pro
;   NAME/KEY: UNSURE
;   LOCATION: 28
;   OTHER INFORMATION: Xaa = Met,Val
;   NAME/KEY: UNSURE
;   LOCATION: 19
;   OTHER INFORMATION: Xaa = Pro,Gln
;   NAME/KEY: UNSURE
;   LOCATION: 53
;   OTHER INFORMATION: Xaa = Ser,Tyr
US-09-621-976-4601

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Query Match 5.8%; Score 344.5; DB 4; Length 75;  
Best Local Similarity 82.6%; Pred. No. 1.9e-14;  
Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

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Qy      1 MEDLDQSPLVSSSDSPRRQPAPFKYQFVREPEDEEEEEEEEEEEDEDLEEEVLERKPA 60  
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Db      1 MEDLDQSPLVSSSDSPRXQPAPFKYQFXREPEDDEE-----EDLEEVLERKPA 49  
  
Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86  
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Db     50 AGLXAAPVXTAPAAGAPLMDFGNDFV 75
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## RESULT 10

US-08-714-741-32  
; Sequence 32, Application US/08714741  
; Patent No. 6500613  
; GENERAL INFORMATION:  
; APPLICANT: Briles, David E.  
; APPLICANT: McDaniel, Larry S.

```

; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

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Query Match          5.3%; Score 316; DB 4; Length 8991;
Best Local Similarity 21.4%; Pred. No. 9.9e-10;
Matches 248; Conservative 138; Mismatches 479; Indels 296; Gaps 52;

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Qy      6 QSPLVSSSDSP-PRPQPAFKYQF-VREPEDEEEEEEEEEDEDEDLEE--LEVLERKPAA 61
      ::|      :| |:| || | :      :|: |: :::: |||      ||      : :::|
Db      7193 EAPAEQPKPAPAPQAPAPKPEKPAPAEQPKPEKTDDQQAEDYARRSEEEYNRLTQQQPPK 7252

Qy      62 GLSAAPVP-----TAPAAG-----APLMDF 81
      || |      | | |      | |
Db      7253 AEKPAPAPKTGWKQENGWYFYNTDGSMGEQAGQYRAAAEGDLAAKQAELEKTEADLKKA 7312

Qy      82 GNDFVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPED---DE 138
      |: |||      || | || || |:|      ||| |      | : : |:|
Db      7313 VNEPEKPAPAPETPA--PEAPAEQPK--PAPAPQAPAPKPEKPAPAEQPKAEKTDDQQAEE 7368

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QY 139 PPAR-----PPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXX 189  
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 Db 7369 DYARRSEEEYNRLTQQQPPKAEKPAPAPKPEQPAPAPKNSKGEQAEQYRSAAGGDLAAKQ 7428  
 QY 190 XKI----MDLKEQPGNTISAGQEDFPSVLLET-AASXPSSLSPLSAASFKEHEYLGNLSTV 244  
 :: ||| : : : | : || | : | : :  
 Db 7429 VELEKTEADLKK-----AVNEPEKPAPAPETPAPEAPAEQPKPAPAPQ----- 7471  
 QY 245 LPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVAN 304  
 | : | : || : | || || : : : ||||  
 Db 7472 -PAPAPKPEKPAEQPK--AEKPADQQAEDYDRRSEEEYNRL--TQQQPPKAEKPAPAPQ 7526  
 QY 305 PREEI-----IVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNE 357  
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 Db 7527 PEQPAPAPKSLKEIDESSEDYVKEGFRAPLQSELDQAKLSKLEEL-----SDKIDE 7580  
 QY 358 KRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQ 417  
 : | : : || || || : : | : || ||||  
 Db 7581 LDAEI-AKLEKDVEDFK-----XSDGEQAGQYLAAAEEDLIAKKA---ELEQ 7623  
 QY 418 TNHEKDSSESSNDDTSFPS---TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTS 474  
 | | | : : : | : || || || || |  
 Db 7624 T--EADLKKAVNEPGKPAPAPAPE-----TPAPEAPAEQPK-----PAP 7660  
 QY 475 ENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYV--TTDNLTKVTEEVVA-- 530  
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 Db 7661 ETPAPAPKPEKPAEQPKPEK-----PADQQAEDYARRSEEEYNRLTQQQPAPA 7709  
 QY 531 -----NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584  
 || : | : : : : : | | | | : : : |  
 Db 7710 QKPEQPAKPEKPAAEPTQPEKDAEIAKLE-KNVEYFKKTDAEQTEQYLA AEKDLADKKA 7768  
 QY 585 SFESEA-----TPSPV-LPDIVMEAPLNSAVPSAGASVIQSSSPLEAS 628  
 | : || || : | | : | | : : : :  
 Db 7769 ELEKTEADLKKAVNEPEKPAAETPAPAPKPEQPAEQPKPAPAPQP-APAPKPEKTDDQQA 7827  
 QY 629 SVNYESIKHEPENPPPYEEAMSVSLKVSGIKEE---IKEPENINAALQETEAPYISIIAC 684  
 : | | | : : | | : || | | : |  
 Db 7828 EEDYARRSEEEYNRLPQQQPPKAEKPAPAPKPEQPVPAEXPEN-----PAPAPKPAXAP 7881  
 QY 685 DLIKETKLSAEPAPDFSDYSEMAKVEQPV-----PDHSELVEDSS-----PDS 727  
 : | : : : | | : | | : | : |  
 Db 7882 QPLKPEEPAEQPKPE-----KPEEPAGQPEPEKPDQQAEDYARRSGGEYNRFPQQ 7933  
 QY 728 EPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMIEYENKEKLSALPPEGG----- 781  
 : | | : : | | | | || : :  
 Db 7934 QPPKAEKPAPAP----KPEQVPAPKTL-----KKAKLAGAKSKAATKKAEL 7977  
 QY 782 KPYLESFKLSLDNTKDTLLP-----DEV-----STLSKK-EKIPLQMEELSTAVYSNDD 829  
 : | || : | : || | || : | : || | : | : : |  
 Db 7978 EPELEKAEAELENLLSTLDPEGKTQDELDKEAAEALNKKVEALPNQVSELEEEELSKLED 8037  
 QY 830 LFISKEAQIRETETFS DSSPIEII DEFPTLISSKTDSFSKLARE----YTDLEVSHKSEI 885  
 | : : | : | : | : | : | : |  
 Db 8038 NL--KDAETNNVEDY-----IKEGLEEAIATKQAELEKTPKELDAAALNELGPDGDEEE 8088

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Qy      886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI--SFSDDFSKNKSATSKVLLLPDVSAL 943
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Db      8089 TPPPEAPAEQPKPEKPAE-ETPAPAPKPEKSADQQAEEYARRSEEEYNRL----- 8138

Qy      944 GHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRD---I 1000
      || : || || | : | : | | : | :
Db      8139 --TQQQ-----PPK-----AEKPAPAPAPKPEQPAPAPKSRGLATKKKLNLAELRIELL 8186

Qy      1001 KKTGV-----VFGASLFLLLS 1016
      || | : || | ||
Db      8187 KKLGLEPGLEKAGAGLGNLLS 8207

```

RESULT 11

US-09-976-594-726

; Sequence 726, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 726

; LENGTH: 2468

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6673549 4295277CD1

US-09-976-594-726

Query Match 5.0%; Score 296.5; DB 4; Length 2468;

Best Local Similarity 21.5%; Pred. No. 2.5e-09;

Matches 264; Conservative 148; Mismatches 459; Indels 355; Gaps 59;

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Qy      2 EDLDQSPLVSSS-DSPPRPQPAFKYQ---FVREP-----EDEE 35
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Db      956 EDGEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGEAEQ 1015

Qy      36 EEEEEEEDEDEDLEEELEV-LERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPL 94
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Db      1016 SEEEADEEDKAEDAREEEYEPEKMEAEDYVMAVVDKAAEAGGAEQYGFLLTPTKQLG-- 1073

Qy      95 PAAPPVAPERQPSWDPSVPSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ 154
      : | | : : | | : | | | | : | | | :
Db      1074 ----AQSPGREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTATSGYT 1120

Qy      155 AEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----D 209
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Db      1121 QSTIEISSEPTPMDEMSTP-----RDVMSDETNNETESPSQEFVNITK 1164

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Qy 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259  
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 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFSRSA 1222  
  
 Qy 260 -----KEVSEKAKTLLIDRDLTEF-----SELEYSEMGS---SFS 291  
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 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPPSKSPSLSPSPSPLEKTPLGERSVNFS 1280  
  
 Qy 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328  
 : : | | : | : : : : | : : | : : |  
 Db 1281 LTPNEIKVSAEAEVAPVSPPEVTQEVVEHCASPEDKTLEVVSPPSQSVTGSAGHTPPYQSP 1340  
  
 Qy 329 ----QQELPTALTCLVKEDEVSSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383  
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 Db 1341 TDEKSSHLPTFV--IEKPPAVPVSEFEFSDAKDENERASVSPMDPEVPDSESPIEKVLSP 1398  
  
 Qy 384 DSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDR 443  
 | : : | | : | | | : : | | :  
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEESKSGKQGSPPDQVSPVSE----- 1447  
  
 Qy 444 SGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDEKK-----IEKK-----A 488  
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 Db 1448 ----MTSTSLYQDKQEGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSP 1503  
  
 Qy 489 QI-----VTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVA--N 531  
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 Db 1504 QIDVSQFGSKEDTKMSISEGTVSDKSATP--VDEGVAEDTYSHMEGVASVSTASVATSS 1561  
  
 Qy 532 MPEGLTPDLVQEACESELNEVTGKTIAYETKMDLVQTSEVMQES-LYPAAQLCP----- 584  
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 Db 1562 FPEPTTDD-VSPSLHAEVGSPPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMSIS 1620  
  
 Qy 585 -----SFESEATPSPVLP-DIVMEAPLNSAVPSAGASVI 618  
 | | : : | | : : | : | : | :  
 Db 1621 PPDFS PKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPDH---PTVGAGVL 1677  
  
 Qy 619 Q-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSGIKEEIKE 664  
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 Db 1678 HITENGPTFVDYSPSDMQDSSLSHKIPPMEEPSYTDNDLSELISVSQVEASPSTSSAHT 1737  
  
 Qy 665 PENINAALQETE----AP-----YISACDLIKE---TKLSAEP-----A 697  
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 Db 1738 PSQIASPLQEDTLSDVAPPRDMSLYASLTSEKVSLEGEKLSPKSDISPLTPRESSPLY 1797  
  
 Qy 698 PDFSDYSEMAKVEQPVPDHSSELVEDSSPDSEPVDLFS----- 734  
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 Db 1798 PTFSDSTSAVK-EKTATCHS----SSSP---PIDAASAEPYGFRAVLFDTMQHHALNR 1849  
  
 Qy 735 DDSIPDVP-----QKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPE 779  
 | | : | : | : | : | : | : | :  
 Db 1850 DLSTPGLEKDSGGKTPGDFSYAYQKPEET-----TRSPDEEDYDYESYEKTTTSDV 1901  
  
 Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSAQIR 839  
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 Db 1902 GGY-YYEKIERTTKSPSDSGYSYE--TIGKTTKTP-----EDGDYSYE--IEKTTTRTP 1950

QY 840 ETETFSDSPIEIIDFPTLISSKTDs---FSKLAREYTDLEVSHKSEIANAPDGAGSLP 896  
 | : | | | | | : | : : | :  
 Db 1951 EEGGYSYD-----ISEKTTSPPEVSGYSYEKTERSRRLLDDISNGYDDS---- 1994

QY 897 CTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPVVSALGHTQAE-IESIVK 955  
 : | | : : ||| : : || | | : | | :  
 Db 1995 -EDGGHTLGDPSSYSYETTEKITSFPESEGYSETSTKTTRTPDTSTYCYETAEKITRTPQ 2053

QY 956 PKVLEKE-----AEKKLPSDTEKE 974  
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 Db 2054 ASTYSYETSDLCYTAEKKSPSEARQD 2079

RESULT 12

US-09-149-476-411

; Sequence 411, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
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; EARLIER APPLICATION NUMBER: 60/043,568  
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; EARLIER APPLICATION NUMBER: 60/043,674  
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; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/047,590  
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; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23



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; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          4.8%;  Score 285;  DB 4;  Length 92;
Best Local Similarity 57.1%;  Pred. No. 1.2e-10;
Matches    52;  Conservative    20;  Mismatches    19;  Indels      0;  Gaps      0;
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QY      1079 NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTLLILALISLFSVP 1138
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Db        2 NAAMVHINRAKLIIIRLFLVEDLVDLSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61

QY      1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1169
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Db        62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92
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RESULT 13

US-08-973-462-8

; Sequence 8, Application US/08973462B  
 ; Patent No. 6191270  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DRUILHE, PIERRE  
 ; APPLICANT: DAUBERSIES, PIERRE  
 ; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES  
 ; FILE REFERENCE: 0660-0125-0 PCT  
 ; CURRENT APPLICATION NUMBER: US/08/973,462B  
 ; CURRENT FILING DATE: 1998-02-06  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/00894  
 ; EARLIER FILING DATE: 1996-06-12  
 ; EARLIER APPLICATION NUMBER: FR 95/07007  
 ; EARLIER FILING DATE: 1995-06-13  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 1786  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide  
 US-08-973-462-8

Query Match 4.7%; Score 276.5; DB 3; Length 1786;  
 Best Local Similarity 20.1%; Pred. No. 2.6e-08;  
 Matches 232; Conservative 201; Mismatches 471; Indels 249; Gaps 50;

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Db	228	EESVEENDEESVEENVEENVEENDDGSVASSVEESIASSVDESIDSSIEENVAPTVE---	284
Qy	84	DFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPAR-	142
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Db	285	EIVAPS-----VVESVAPSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAEN	338
Qy	143	-----PPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQ	198
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Db	339	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	398
Qy	199	PGNTISAGQEDFPSVLLETAAS-----XPSLSPLSAAASFKEHEYLGNLSTVLPT-EGTL	251
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Db	399	VAENV---EESVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESV	455
Qy	252	QENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVI-----VANP	305
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Db	456	EENVEESVAENVEESVAENVEESVAENVEESVAE-NVEESVAENVEESVAENVEESVAEN	514
Qy	306	REEIIVKNKDE-----EEKLVSNNILHX-----QQELPTALTKLVKED-----EVV	346
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Db	515	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	574
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYA-----DFKPFERVWEVKDSKEDSDMLAAGGKIESN	401
		:   : :     :       : :         :	
Db	575	VAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEES-----VEEN	626

Qy 402 LESKVDKKCFADSLEQTNHE--KDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATE 459  
 :| | |::|: | :| : | : | | : | :|  
 Db 627 VEESV-----AENVEESVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVA----PSVVE 677

Qy 460 SIATNIFPLLEDPTSENXTDE--KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVT 517  
 |:| | :|: || : : :| | : | | : || | |  
 Db 678 SVA----PSVEESVEENVEESVAENVEESVAENVEESVAENVEES---VAENVEEIVAPT 730

Qy 518 TDNLTKVT-EEVVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTS--EVMQ 573  
 : : | |::| | : | : | | : | : | : | : | : :  
 Db 731 VEEIVAPTVEEIVAPSVVESVAPS-VEESVEENVEESVAENVE-ESVAENVEESVAENVE 788

Qy 574 ESLYPAAQ--LCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVN 631  
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 Db 789 ESVAPTVEEIVAPSVVEESVA-PS-----VEESVAENVATNLSNLLSNLLGGIETEEIK 841

Qy 632 YESIKHEPENPPP-----YEEAMSVSLKV-SGIKEEIKE----PENINAALQETEA 677  
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 Db 842 -DSILNEIEEVKENVVTILENVEETTAESVTTFSNILEEIQENTITNDTIEEKLEELHE 900

Qy 678 PYISIA-----CDLIKETKLSAEPAPDFSDYSEMA--KVEQPVPDHSSELVED 722  
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 Db 901 NVLSAALENTQSEEEKKEVIDVIEEVK--EEVATTLIETVEQAEKSANTITEIFENLEE 958

Qy 723 SSPDS-----EPVDLFSDDSDIPDVPQKQDETVMVVKESLTET----- 759  
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Qy 760 -----SFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK 810  
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 Db 1019 ENLLTGMFRSIETSIVIQSEEKVDL-----NENVVSSILDNIENMKEGLL-NKLENISST 1072

Qy 811 E-----KIPLQMEE-----LSTAVYSNDDL- 831  
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 Db 1073 EGVQETVTEHVEQNVYVDVDPAMKDQFLGILNEAGGLKEMFFNLEDVFKSESVDITVEE 1132

Qy 832 -----ISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSSFSLKAREYTDLEVSHKSEIA 886  
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 Db 1133 IKDEPVQKEVE-KETVSIIEEMENIVDVLEEEKEDLTDKMIDAVEESIEISSDSKEETE 1191

Qy 887 NAPDGAG--SLPCTELPHD-----LSLKNIQPK-VEEKISFSDDFSKNGSATSKVL 934  
 : | || : : | ||| : : : : : | ||: :  
 Db 1192 SIKDKEKDVSLVVEEVQDNDMDSEVEKVLELKNMEEELMKDAVEIND-----ITSKLI 1244

Qy 935 LLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPSDTE-----KEDRSPSAIFSADLGKT 989  
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 Db 1245 ---EETQELNEVEAD---LIKMEKLKELEKALSSEDSKEIIDAKDDTLEKVIEEEHDITT 1298

Qy 990 SVVDLLYWRDIKK 1002  
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 Db 1299 TLDEVVELKDVEE 1311

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; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1601
; TYPE: PRT
; ORGANISM: C. elegans
US-09-345-473E-40
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Query Match          4.5%; Score 267.5; DB 4; Length 1601;
Best Local Similarity 20.5%; Pred. No. 8e-08;
Matches 229; Conservative 134; Mismatches 376; Indels 377; Gaps 56;
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Qy      29 REPEDEEEEEEEEE-----EDEDLEDLEEVLERKPAAGLSAAPVPTAPAAGA 76
      | :|| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      462 RAKEEEERIREAAEIKEELRLRAEAKEKEKERLEK-ERLEKKAAAAAANPNPTP----- 515

Qy      77 PLMDFGNDFVPPAPRGP-----LPAAPPVAPE-----RQPSWDPS-PVS--STVPAPSP 122
      :|| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      516 -----IPPTPATPHSSAQQQPIPPPLSTQTSAEIQQSAQQQPSVPVTMIANIPAMSP 566

Qy     123 LSA---AAVSPSK----LPEDDEPPARPPPPPPASVSPQAEPVW---TPPAPAP--AAPP 170
      || :||: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     567 TSAQPQFVLSPTSAAVPVPTTMIHVPKPSEIPVQNVATTAAPVAANNVPPSPAPFKTEDI 626

Qy     171 STPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAG-QEDFPSVLLETAASXPSLSPLSA 229
      || : | | | | | | | | | | | | | | | | | | | | | | | |
Db     627 QTPTLAQ-----NTVPTISTDASGLVINTPASIASPSPAPS 663

Qy     230 ASFKEHEYLGNLSTVLP-----TEG-----TLQENVSEASKEVSEKAKTLLIDRDLT 276
      |: : : | | | | | | | | | | | | | | | | | | | | | | | |
Db     664 AT----DVASTTAPVTPAPTPTTTTGDGAAAASTTTENKEEKRKSNKRKVVM EILGCDES 719

Qy     277 E-----FSELEYSEMGSFSVSP-----KAESAVIVANPREEIIVK 312
      |: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     720 RNFALVSCRLDTSHKSVTFQFAPGTDKPCTIATKLLAEDCLLKVVHIVEAQLGEVIQLI 779

Qy     313 NKDEEE----KLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMRE 368
      | | :: | | : :| | :| :: :| | | | : :: :
Db     780 NSDGKKGVGTKLAT--VLDPNSTEPPTITAVMPKD----SSAATASNTKPKIEI----- 827

Qy     369 EYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESN 428
      |: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     828 -----EKTPTTRDASQE-----PNNVQVTNVRKVSQESN 856

Qy     429 DDTSPSTPEGIKDRSGAYITCAPFN-----PAAT---ES 460
      : | | | | | | | :| | | | | | | | | | | | | | | | | |
Db     857 AE-SVQSIP-----RPGGIIVMSPTNQTD SAPPTGAAAKPSRFQVTKSADPIATPISSS 910

Qy     461 IAT-NIFPLLEDPTSENXTDEKKIEEK-KAQIVTEKNTSTKTSNPFVAAQDSETDYVTT 518
      |:| : :|: | | | | : ||::| | : | : : :| |
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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/978,277A
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/665,401
;   FILING DATE:  18-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Clark, Richard S
;   REGISTRATION NUMBER:  26,154
;   REFERENCE/DOCKET NUMBER:  A30558 - 165/34008
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  212-408-2558
;   TELEFAX:  212-765-2519
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1596 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FRAGMENT TYPE:  internal
;   ORIGINAL SOURCE:
US-08-978-277A-4

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Query Match          4.5%;  Score 265;  DB 4;  Length 1596;
Best Local Similarity 21.3%;  Pred. No. 1.1e-07;
Matches 232;  Conservative 145;  Mismatches 422;  Indels 288;  Gaps 47;

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Qy      2 EDLD--QSPLVSSSDSPPRPQPAFKYQFVREPEDE-----EEEEEEEEDEDEDLEELEV 54
      |:|:  :|  :||:|  |  :|  ||::  ||  :  :  |
Db      620 EELEKVKSATLSSTDST-----VSEMQDEVKTVGEEQKPEEPKRRVDTSVSWEA 668

Qy      55 LERKPAAGLSAAPVPTAPAAGAPL-----MDFGNDVFPPAPR----- 91
      |  ::  |  ::  |  |  :  ||  ||  :  :
Db      669 LICVGSSKKRARKASSSDDEGGPRTLGGDSHRAEEASKDKEAGTDAVPASTQEQQDAQGS 728

Qy      92 -GPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAVSPSKLPEDDEPPARPPPPPPAS 150
      |  ||  |  |  :|:  |  :|  |  ||  |  |  :
Db      729 SSPEPAGSPSEGEVSTWE-----SFKRLVTPRKK---SKSKLEEKAEDESS--VEQLSTE 778

Qy      151 VSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAG---- 206
      :  |  |  |  :  |  |  :|  |  |  :  :  |
Db      779 IEPSREESWV-----SIKKFIPGRRKKRA-----DGKQEQTATVEDSGPVEI 819

Qy      207 QEDFPSVLLETAASXPSLSPLSAAFSKEHEYL---GN-----LSTVLPTEGTLQENVSE 257
      ||  |:|  |  :|  ||  :  |  |  :  ||  |  |  :|  |
Db      820 NEDDPNV-----PAVVPLSEYNAVEREKMEAQGNTELPQLLGAVYVSE-----E 863

Qy      258 ASKEVSEKAKTLLID--RDLTEFSELEYSEMGSSFVSVPKAESAVIVANPREEIIVKNKD 315
      ||  :  :||  |  :|  |  |  :  :|  :  |  |  :|  :
Db      864 LSKTLVHTVSVVAVIDGTRAVTSVEERSPSWISASVT-EPLEHTAGEAMPPVEEVTEKDII 922

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:00:14 ; Search time 25.1547 Seconds  
(without alignments)  
4504.667 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	787.5	13.3	776	2	A46583	neuroendocrine-spe
2	688	11.6	208	2	I60904	neuroendocrine-spe
3	671	11.3	267	2	A60021	tropomyosin-relate
4	528	8.9	2484	2	T26216	hypothetical prote
5	519.5	8.8	2607	2	T26215	hypothetical prote
6	340.5	5.7	222	2	T26213	hypothetical prote
7	331	5.6	7962	2	I38346	elastic titin - hu
8	325.5	5.5	5327	2	T13564	microtubule-associ
9	324.5	5.5	865	2	A47282	calcium-binding pr
10	320.5	5.4	873	2	A47283	calphotin - fruit
11	299.5	5.1	3488	2	T34418	hypothetical prote
12	299	5.0	3924	2	S37431	ankyrin 2, neurona
13	290.5	4.9	1274	2	T16251	hypothetical prote



14	289	4.9	2364	2	A56577	microtubule-associ
15	289	4.9	2464	1	QRMSP1	microtubule-associ
16	287.5	4.9	971	2	T19431	hypothetical prote
17	285.5	4.8	1621	2	A82255	hypothetical prote
18	278	4.7	1948	2	S00485	gene 11-1 protein
19	274	4.6	3507	2	T34513	hypothetical prote
20	272.5	4.6	1829	2	T24583	hypothetical prote
21	272.5	4.6	2361	2	T25752	hypothetical prote
22	271	4.6	2187	2	T30826	nascent polypeptid
23	270	4.6	1230	2	T22458	hypothetical prote
24	267.5	4.5	1851	2	T19964	hypothetical prote
25	263.5	4.4	2409	1	A60979	versican precursor
26	262.5	4.4	6642	2	T29757	protein UNC-89 - C
27	261	4.4	1558	2	B71603	RESA-H3 antigen PF
28	260.5	4.4	3381	2	T42389	versican precursor
29	259.5	4.4	1828	2	A40115	microtubule-associ
30	258	4.4	1616	2	G64242	cytadherence-acces
31	257.5	4.3	5170	2	T15348	hypothetical prote
32	256	4.3	990	2	I51618	nucleolar phosphop
33	256	4.3	1634	2	T26517	hypothetical prote
34	255.5	4.3	1684	2	JW0057	gravin - human
35	253	4.3	1189	2	S56852	hypothetical prote
36	252.5	4.3	1224	2	T14007	microtubule-associ
37	252	4.3	4377	2	A55575	ankyrin 3, long sp
38	250.5	4.2	1824	1	QRHUMT	microtubule-associ
39	250.5	4.2	1830	2	A37981	microtubule-associ
40	248	4.2	1825	2	S13507	microtubule-associ
41	248	4.2	1890	2	T04556	hypothetical prote
42	248	4.2	3421	1	WZBEB6	367K tegument prot
43	246	4.2	1110	2	I51116	NF-180 - sea lampr
44	244.5	4.1	1029	2	T30351	mucin-like protein
45	243	4.1	1320	2	JC5630	TCOF1 protein - mo

#### ALIGNMENTS

##### RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 421-776 <ROE2>  
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309  
C;Genetics:  
A;Gene: GDB:RTN1; NSP  
A;Cross-references: GDB:203968; OMIM:600865  
A;Map position: 14q21-14q22

Query Match 13.3%; Score 787.5; DB 2; Length 776;  
Best Local Similarity 31.9%; Pred. No. 3.1e-25;  
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

Qy	588	ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY----	632
		: :    :   : :   :   :	
Db	141	EELGTPGPSLDPVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDIT	200
Qy	633	--ESIKHEPENPPPYEEA-----MSVSLKVSIGIKEEIKEPENINAAL-----QET	675
		:  : ::    : :    ::     : : :	
Db	201	RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST	259
Qy	676	EAPYISIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED	722
		:     : : : :   : :	
Db	260	FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK	309
Qy	723	SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF	761
		:          :      : :  :	
Db	310	PSPDPTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQKGKSISEDELITAIKEA-----	363
Qy	762	ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS	821
		:      : :           : : :	
Db	364	-KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA	403
Qy	822	TAVYSNDDLFISKEAQIRETETFSDSPIEIDEFP----TLISSKTDSEFS-----	868
		::         :     :	
Db	404	SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP	444
Qy	869	-----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDSLKNIQPKVEEKISFSD	921
		:    :  : :   : :   :	
Db	445	ASPSIQYSILREERAELDSELIIESCDASSAS-----EESPKREQDSPMPKPSALD	496
Qy	922	DF-----SKNGSATSKVLL-----LPPDVSA LGHTQAEIESIVKP	956
		:                   : :	
Db	497	AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQGPPELPPGDGAL-----EPETPMLP	551
Qy	957	KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK	1001
		:   : :   :   :     :	
Db	552	-----RKPEEDSSSNQSPAATKGPGPLGPGAPPPLLF---LNKQKAIDL YWRDIK	599
Qy	1002	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1061
		:   :   :             :	
Db	600	QTGIVFGSFLLLFLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKA	659
Qy	1062	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1121
		: :   :   : : :     :	
Db	660	YLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALF	719

QY 1122 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
| | | | :  
Db 720 NGLTLLMAVVSMTFLPVVVKHQEQIDQYLGLVRTHINAVVAKIQAQIPGAKRHAE 776

## RESULT 2

T60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 11.6%; Score 688; DB 2; Length 208;  
Best Local Similarity 67.5%; Pred. No. 6.2e-22;  
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

Qy           988 KTSVVDLLYWDRDIKKTGVVFGASLFLLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 1047  
             | :   :|||||||::||:| | | || | |:| | | | | | | | | :  
Db           18 KSQAIDLLYWDRDIQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 77

Qy            1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107  
             ||:||:|||||:||||| |: :||: |:|||::     :|| |:||||||| |||||

Db            78 QAVOKTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKF 137

Qy 1108 AVLMWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQ 1167  
| | | | : | | | | | | | | | | : | : | : | : | : | : | | | | : | | | : | | |  
Db 138 AVL MWLLTYVGALFENGLTLLMLAVVSMFTLPVVYVKHQAIQDQYLGLVRTHINAVVAKIQ 197

Qy 1168 AKIPGLKRKAE 1178  
||| | | |  
Db 198 AKIPGAKRHAEE 208

### RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text\_change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991



Qy 39 EEEEEED-----EDEDLEEEVLERKPA-----AGLSAAP----- 67  
 :||| | | : | : | : | :  
 Db 1454 NQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDVDASDVNEQDEESTLKIL 1513  
 Qy 68 --VPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAP--ERQPSW----- 108  
 | : | : : | | | | : | | | | :  
 Db 1514 KVVFPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV 1569  
 Qy 109 -----DPSPVSSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW 159  
 | | | | | | : | | | | | : | :  
 Db 1570 TESEISEMAPQVSESTCPIPEPL-----ADLKLPVEDDEKTPEPEPVVPGQVQERIPIE 1624  
 Qy 160 TPPAPA-PAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVL--LE 216  
 | | | | | : : | | | :  
 Db 1625 VEQAPTIPQRPPRAP-----KSELPKVAKPLD 1651  
 Qy 217 TAASXPSLSPLSA-----ASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLL 270  
 : | : | : : : | : | | | : : : : | : |  
 Db 1652 DSKSRVRFAPLNIKLGRITYSEEQQKELVESLERPL-TIITQQKPPEKPTEDIG--ALSPL 1708  
 Qy 271 IDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQ 330  
 | | : | : : | : : : | | | : : | |  
 Db 1709 SPNTLAEEYEEVPMMDMQS-----VPHSPQE-----KQEEIEALSEII----- 1745  
 Qy 331 ELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK---PFERVWEVKDSKE 387  
 | | | : : | | : | | : | : | : | : | :  
 Db 1746 EEPQAMKEVEKPVE-SAPEKDNESLEAPEI-INEPIRRVLVETKIMGPGKSLNEDNDDDD 1803  
 Qy 388 D-SDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESS---NDDTSFPSTPEGIKD 442  
 | | : | : | : | : : | | : : | | | | : | : | :  
 Db 1804 DGSECLDSIGDLS---ERTIQR--FNTSIDDPSIRRDSFSSISSFGDRQKFRTAIENIRQ 1858  
 Qy 443 RSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSN 502  
 | | : : : : : | : : | |  
 Db 1859 -----DLLPFQSSVSQYLRRSPNP-----SQQLLVTN----- 1885  
 Qy 503 PFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETK 562  
 : | | : | : | | | | : : : | : : | : : |  
 Db 1886 ----LSMDSPSD--LSPNAPPVGFENTAQFLEKLQQE-DRPSAEGSIDSSGFQKVDHE-- 1936  
 Qy 563 MDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS 622  
 : | | | | : | | | | : : : | : : | : : |  
 Db 1937 -----GLDEFAAPP-----VHDPMQKSVFGSLGSDDMKPGS 1967  
 Qy 623 SP-----LEASSVNYESIKHEPENPPPYYEAMSVSLKVSGIKEEIKEPENIN-----AAL 672  
 : | : | | : : | : | : | : | : | : | :  
 Db 1968 QDDGFVFIERNAN-----EATLKKNQKMSSHNDVIEKNYFNDNAPTAAL 2013  
 Qy 673 QETEAPYISIACDLIKETKLSAEPAPDFSDYSEMA-----KVEQPVPDHSEL 719  
 | : | | | : : | | : | : | | : | : | :  
 Db 2014 --LESPIAEEARKLVQDAVESA-----SEYKKQAVDSGDEIGRELLDNVEQKIEQVKEP 2065  
 Qy 720 VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE 779  
 : | : | | | : | : : | : | : | : | :  
 Db 2066 IVDSL--HKAYDGVGDFVHETV PNAVD D FVREA EKQLPESPVPEKIE-----TPE 2113

Qy	780	GGKPYLESFKLSLDNTKDTL--LPDEVSTLSKKEKIFLQMEELSTAVYSNDDLFIKEAQ	837
Db	2114	-----PLVDIHDTVDKVHDEVNDFLRREPTP-PFETDDVAPLSDDKPQFGNQTP	2161
Qy	838	IRETETFSDDSSPIEIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPC	897
Db	2162	EEDETTFDRKGPLTIPEEVEKAAAAQNNDLD----DFDPLVTSNTGAAFGAAGVAAAA--	2215
Qy	898	TELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLLPPDVSA LGHTQAEIESIVKPK	957
Db	2216	-----VESLTEEM-----FGH--QKFETVPRPP	2237
Qy	958	VLEKEAEKKLPDSTEKEDRSPSAIFSADLG-----KT--	989
Db	2238	T-----PPKDISDEDVKPSTV---NLGPSHHHSHPSPPHHSILKHHGDAWIDFKTVP	2286
Qy	990	-SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIO	1048
Db	2287	PCVLDVIYWRDAKKSIVLSLALLVLFVLAKYPLLTVVITYSLLLALGAAAGFRVFKKVEA	2346
Qy	1049	AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFA	1108
Db	2347	QIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFG	2406
Qy	1109	VLMWVFTTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA	1168
Db	2407	LVLWSLTYIASWFSGFTLAILGLLVGVFSVPKYESNQEAIDPHLATISGHLKKNVQNIIDE	2466
Qy	1169	KIPGLK	1174
Db	2467	KLPFLR	2472

Qy	1	MEDLDQSLVSSSDSPPRPQPAFKYQFVREPEDEEE-----EE	38
Db	1397	LEKVEVQP--DLSQNSPAPHKIIDLHF-NIPKDHEDYGNDYVFPFGTESSEESQKADGNQE	1453
Qy	39	EEEEED-----EDEDLEELEVLERKPA-----AGLSAAP-----	67
Db	1454	NQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDVDASDVNEQDEESTLKIL	1513
Qy	68	--VPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP--ERQPSW-----	108
Db	1514	KVVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV	1569
Qy	109	-----DPSPVSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW	159
Db	1570	TESEISEMAPQVSESTCPIPEPL-----ADLKLPVEDDEKTPEPEPVVPGQVQERIPIE	1624
Qy	160	TPPAPA-PAAPPSTP-----AAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQE---	208
Db	1625	VEQAPTIPQRPPRAPKSELPKVAKPLDDSKS-----RVRFAPLNIKLGRTYSEEQQKEL	1678
Qy	209	----DFPSVLLETAASXP-----SLSPLSAASFKEHEY--LGNLSTVLPTTEGTLQEN	254
Db	1679	VESLERPLTII-TQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMMDMQSVPHSPQEKQEE	1737
Qy	255	VSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVK--	312
Db	1738	I-EALSEIIEEPQAM-----KEVEKPVESAPEKDNESLEAPEIINEPIRRVLVETK	1787
Qy	313	-----NKDEEEKLVSNNILHXQQELPTALTCLVKEDDEVVSSEKAKDSFNEKRVAVEA	364
Db	1788	IMGPGKSLNEDNDDDDDGSECLDSIGDL-----SERTIQRFN---TSIDD	1829
Qy	365	P--MREEYADFKPFERVWEVKDSKED--SDMLAAGGKIESNLESKVDKCFADSLEQTNH	420
Db	1830	PSIRRDSFSSISSFGDRQKFRTAIENIRQDLLPFQSSVSQYLRSNP--SQQLLVTNL	1886
Qy	421	EKDSSESNDDTSFPSTPEGI-----KDRSGA--YITCAPFNPAATESIATNIF	466
Db	1887	SMDSPS---DLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSIDSSGFEEKVDHEGLDEF	1943
Qy	467	PLLEDPTSEN-----XTDEKK-----IEEKKAQIVTEKNTSTKTSNPPFFVAAQDS	511
Db	1944	PPVHDPMQSKSVFGLSGDDMKPGSQDDGVFIERNEANEATLKNQKMSSHNDVIEKNY	2003
Qy	512	ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV-TGTKIAYE----TKMDLV	566
Db	2004	FNDNAPT---AALLESPIAEEARKLVQDAVESASEYKKQAVDSGDEIGRELLDNVEQKIE	2060
Qy	567	QTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLE	626
Db	2061	QVKEPIVDLSLHKAYDGVGVFVH-ETVNAV-DDFVREAE-----	2097
Qy	627	ASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAAALQETEAPYISACDL	686
Db	2098	-----KQLPESPVP-----EKIETPE-----PLVDIHDTV	2122

Qy 687 IK-----ETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSDIPDV 741  
 | : | | | | : | : | : | :  
 Db 2123 DKVHDEVNDNFLRREPTPPFE-----TDDVAPLSDDKPQFGNQ----- 2160

Qy 742 PQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLP 801  
 : | | | | | : | : | : | :  
 Db 2161 -PEEDETTFDRKGPLT-----IP 2177

Qy 802 DEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDDSSPIEIIDFPTLIS 861  
 : | | : | : | : | : | : | :  
 Db 2178 EEV-----EKAAAAQNND-----LDDFDPLVT 2199

Qy 862 SKT-----DSFSKLAR-----EYTDLEVSHKSEIANAPD 890  
 | | : | : | : | : | : | :  
 Db 2200 SNTGAAFGAAVGAAAAVESLTEEEMFGHQKFETVPRPPTPPKDISDEDVK-PSTVNLGPS 2258

Qy 891 GAGSLPCTELPHD-----LSLKNIQPKVEEKIS-----FSDDFS 924  
 | | : | : | : | : | : | :  
 Db 2259 HHHSHSPSS--PHHSILKHHGDAWIDFKTVPPCAQNAFSPGEIMFLLAFFVYLSCFASFFS 2316

Qy 925 KNGSATSKVLLL-----PPDVSALG----- 944  
 | : : | : | : | : | :  
 Db 2317 KSLPLLDNLLSLVVYLSISLIHVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNI 2376

Qy 945 --HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKK 1002  
 : : | | | | | | | | : | : | : | : | :  
 Db 2377 VLRVGLNVALVVGVAWSAHEAYKLTKS-----SGVLRKKEVLVDVIYWRDAKK 2423

Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1062  
 : | : | : | : : : | | | | : : | : | : | : | :  
 Db 2424 SAIVLSLALLVLFVLAKYPLLTVTYSLLALGAAAGFRVFKKVEAQIKKTSEHPFSEI 2483

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVETVVGALFN 1122  
 | : : : | | : : : | | : : : | : : : | : : | : : | : :  
 Db 2484 LAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGVLVLSLTYIASWFS 2543

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 1174  
 | | | | : : | | : | : | : : : | : | : | :  
 Db 2544 GFTLAILGLLGVSVPKVVYESNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

# RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:



```

Query Match      5.7%; Score 340.5; DB 2; Length 222;
Best Local Similarity 32.4%; Pred. No. 1.4e-07;
Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;

Qy      972 EKEDRSPSAIFSADL-GKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 1030
      :| : |: : : | || ::|:|||| ||: :| :| :| | : ::| |
Db      9 KKYSKQPTWVWPATDFPGK--ILDVIYWRDAKKSAILVLSALLVLFVLAKYPLLLTVVTYSL 66

Qy     1031 LALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIK 1090
      | |      |:::| | |:::| || | : : :| | :: : | |
Db     67 LLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFEVEHATCIAN 126

Qy     1091 ELRRLFLVDDLVDLSLKFAVLMWVFYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 1150
      ::::| |: ::::| ||:| ||| |: :||| :|| :| ||
Db     127 KLKKLVFVESPLESIKFGVLVWSLTYIASWFSGFTLAILGLLGVFSPKVEYESNQEAIDP 186

Qy     1151 YLGLANKNVKDAMAKIQAKIPGLK 1174
      :| : :::| | |:| |
Db     187 HLATISGHLKNVONIIDEKLPFLR 210

```

Query Match 5.6%; Score 331; DB 2; Length 7962;  
Best Local Similarity 20.0%; Pred. No. 4.7e-05;  
Matches 235; Conservative 144; Mismatches 404; Indels 392; Gaps 48;

Qy	32	EDEEEEEEEEEDEDEDLEELE--VLERK---PAAGLSAAPV-----PTAPA	73
		:               :       : :	
Db	6176	EEEEEEEEEAEVTEYEVMEEPPEEYVVEEKLHIISKRVEAEPAEVTREQKKIVLKP KIPA	6235
Qy	74	AGAPLMDFGNDFVPPAPRGPLPAAP-PVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSK	132
		:   :     :     :	
Db	6236	K-----IEEPPPAKVPEAPKKIVPEKK-----VPAPVP-KKEKVPPPK	6272

Qy 133 LPEDDEPPA---RPPP-----PPPASVS-----PQAEPVWTPPAPAPAAPPS-TPAA 175  
:|: : | : || | || | : | | | | : |  
Db 6273 VPEEPKKPVPEKKVPPKVIKMEELPAKVTEKHMQITQEEKVLVAVTKEAPPKARVPEE 6332

Qy 176 PKRRGSSGAVVXXXXKIMDLK----EQPGNTISAGQEDF---PSVLLETAASXPS-LSPL 227  
||| |:: || |:: :: : | : | : :  
Db 6333 PKR-----AVPEEKVLKLPKREEEPPAKVTEFRKRVVKEEKVSIEAPKREPQPIKEV 6385

Qy 228 SAASFKEHEYLGNLSTVLPTEGTLQEN-VSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286  
: || | |::| || :| : : : | || | : |  
Db 6386 TIMEEKERAY-----TLEEEAVSVQREEEYEEYE----EYDYKEFEEYEPTTEE 6429

Qy 287 GSSFS-----VSPKAESAVIV--ANPREEI 309  
: || | : : | | : :  
Db 6430 YDQYEEYEEERYERYEEHEEYITEPEKPIPVKPVPEEPVPTKPKAPPKVLKKAVPEEKV 6489

Qy 310 IV----KNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAP 365  
| | | : : : : : | | : | | || |  
Db 6490 PVPIPKKLKPPPPKVPPEEPKKVFEEKIHSITK--REKEQVTEPAKVPMKPKRVVAEEK 6547

Qy 366 MREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE 425  
: : | || | : : | : : : : | : || : : |  
Db 6548 VVPRKEVAPPVRVPEVPKELEPEEV-----AFEEEVVTHVE-EYLVEEEEEEYIHEEE-E 6600

Qy 426 SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSXTDEKKIEE 485  
: : | | : : | | | : : | | : : || ||  
Db 6601 FITEEEVVPVIPVKVPE-----VPRKPVPEEKKVPVPVPPKKEAPPKVPPEVPKKPEE 6652

Qy 486 KKAQIVTEKNTSTKTSNPPFF-----VAAQDSETDYVTTDNL----- 521  
| : : : | | : : | : :  
Db 6653 KVPVLIPKKEKPPPAKVPEVPKKPVPEEKVPVPVPPKVEAPPKVPPEVPKKPVPEKKVPV 6712

Qy 522 -----TKVTEEVVANMPEGLTPDLVQACESELNEVTGKIAYETKMDLVQTSEV 571  
|| | : || | | : | : : | : | || ||  
Db 6713 PAPKKVEAPPKVPPEVPKKLIPEEKKPTVPKKVEAPPPKVPKKREPVPVPVALPQEEEV 6772

Qy 572 M-QESLYPAAQLCPSFEESEATP----- 593  
: : | : : | || | |  
Db 6773 LFEEIIVPEEEVLP--EEEEVLPEEEVLPEEEVLPEEEIIPPEEEVPPEEEYVPEEE 6830

Qy 594 -----SPVLPDIVMEAPLNSAVPSAGASVIQ-----PSSSPLEASSVNYESI- 635  
||| : : | : : || | : | | : |  
Db 6831 EFVPEEEVLPEVKPKVPVPAPVPEIKKKVTEKKVIPKKEEAPPKVPPEVPKKVEEKRII 6890

Qy 636 --KHE-----PENPPPYEEAMSVSLKVSGIKEEI---KEPENIN 669  
| | || || || || : : || |  
Db 6891 LPKEEEVLPEVTEEPPEEPISEEEIPEEPPSIEEV-----EEVAPPRVPEVIK 6939

Qy 670 AALQETEAPYISIACDLIKETKLSAEPAPDFS DYSEMAKVEQVPDPHSELVEDSSPDSEP 729  
| : | | : | | || : : : | : : |  
Db 6940 KAVPEAPTVP-----PKKVEAPP-----AKVSKKIPEEKVPVPVQKKEAPP 6980

Qy 730 VDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK 789  
: : || : | : || | | : || | :  
Db 6981 A-----KVPEVPKKVPEKKVLV-----PKKEAVPPAKGR----- 7009

```

Qy      28 VREPEDEEEEEEEEEE---DEDEDLEELEVLERKPAAGLS-----AAPVPTAPAAG 75
      : : :||| |:| | | | : | | : :: | | | :
Db      1277 MEQVKDKKEEHEQKIESGIITEKEAKKSASTPEEKETSDITSDELPAQLADPTTVPPKSA 1336

Qy      76 APLMDFGNDFVPPA-----PRGPLPAAPPV-APERQPSWDPSVPSSTVPAPSPLSAA 126
      | |: || : | || ||| : ||::| | ||
Db      1337 KDREDTGSIESPPTIEEAIEVEVQAKQEAKQKVPAPAEAAIKTEKSPLASK-ETSRPESAT 1395

Qy      127 AVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPA-----APK 177
      : || | | |: :| : | | : | : | |
Db      1396 ----GSVKEDTEQTKSKKSPVPSRPESEAKDKKSPFASGEASRPESVAESVKDEAGKAES 1451

Qy      178 RRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----DFPSVLLETAASXP-SLSPLSA 229
      || | : || | | : | | | || | |:| |

```

Db 1452 RRESIAKTHKDESSLDKAKEQESRRESIAESIKPESGIDEKSALASKEASRPESVTDKS- 1510  
 Qy 230 ASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSS 289  
 || : : | | | : ||| | : : | | | : :  
 Db 1511 ---KEPSRRESIAESLKAESTKDEKSAPPSKEASRPESVSVKDETEKSKEPSRRESIA 1567  
 Qy 290 FSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSN---ILHXQQELPTALTCLKVKEDEVV 346  
 | | | : | | : | | | | : : | : : | : :  
 Db 1568 ESAKPPIEFRE-VSRP-ESVIDGIKDESAKPESRRDSPLASKEASRPESVLESVKDEPIK 1625  
 Qy 347 SSEKAK-----DSFNEKRVAVE-APMREEYADFKPFFERVWEVKDS--KEDSDMLAAGGKI 398  
 | : | : : : | : | : : | : | : | : | : | :  
 Db 1626 STEKSRRESVAESFKADSTKDEKSPLTSKDIS-RPESAVENVMDAPFKETS RPESAVGSM 1684  
 Qy 399 ESNLESKVDKKCFADSLEQTNHE--KDSESSNDDTSFP-STPEGIKDRSGAYITCAPFNP 455  
 : || : | | : : : | | | | | | | |  
 Db 1685 KDESMSK-----EPSRRESVKDGAAQSRERSRPASVAESA--GADDLKELSRP 1732  
 Qy 456 AATE-----SIATNIFPLLEDPTS-----ENXTD--EKKIEEKKAQIVTEKN--TSTK 499  
 : | : | : | : | : | | | : : | | : | :  
 Db 1733 ESTTQSKEAGSIKDEKSPLASEEASRPASVAESVKDEAEKSKEESRRESVAEKSPLPSKE 1792  
 Qy 500 TSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMP----EGLTPDLVQEACESELNEVTGT 555  
 | | | : | | | | | | | | : : |  
 Db 1793 ASRPASVA--ESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDE----AE 1845  
 Qy 556 KIAYETKMDLVQTSEVM--QESLYPAAQLCPSFEESEATPSPVLPDIVME-APLNSAVPS 612  
 | | : : | : : | : : : : | : | : | | |  
 Db 1846 KSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEAS 1905  
 Qy 613 AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEI---KEPENIN 669  
 ||| : | | : : | : | : : | : | |  
 Db 1906 RPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRE 1965  
 Qy 670 AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEP 729  
 : : : | | | | : | : | | | : | |  
 Db 1966 SVAEKSPLP-----SKEASRPASVAESIKDEAEKSKEE----SRRESVAEKSP---- 2009  
 Qy 730 VDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIE--YENKEKLSALP-PEGGKP--Y 784  
 : | : | | : : : : | | : : | | | : |  
 Db 2010 -----LPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASV 2058  
 Qy 785 LESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQME-----LSTAVYSNDDLFI SKEAQIRE 840  
 | | | : : | : | | | | : | | : | | |  
 Db 2059 AESIKDEAEKSK-----EESRRESAAEKSPLPSKEASRPASVAESVKDEADKSKEESRR- 2112  
 Qy 841 TETFSDDSPIEII--DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT 898  
 | : : | : | : | : : | : | | | : | :  
 Db 2113 -ESMAESGKAQSIKGDQSPLKEVSRPES---VAESVKDDPVKSK-EPSRRESVAGSVTAD 2167  
 Qy 899 ELPHDLSLKNIQPKVEEK-----ISFSDDFS KNGSATS KVL LPPDV SALGHTQAE 949  
 | : : | : | | : | | | : :  
 Db 2168 -----SARDDQSPLESKGASRPESVVD SVKDEAEKQES-----RRESK 2205  
 Qy 950 IESIVKPKVLEKEAEKKL-----PSDTEKEDR-SPSAIFSADLGKTSVVDLLYW---RDI 1000  
 | : : | : : | : : : : | : : | : : | |  
 Db 2206 TESVIPPKAKDDKSPKEVLQPVSM TETIREDADQPMKPSQAESRRESIAESIKASSPRDE 2265

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Qy      293 SPKAESAVIVAN-----PREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDDEVVS 347
        :|      | :||      | |||      :| : | :| ||:
Db      195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVVA 234

```

Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407  
: | : | | | | | : : : | |  
Db 235 T---KPLAAAEFVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280

Qy 408 KKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467  
| | : : | : | | | |  
Db 281 -----ASTEPFV---AAATLTAPETPAL----- 301

Qy 468 LLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527  
| : | | | | | | | |  
Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579  
| | | : | : | : | | : | | : | | : | |  
Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371

Qy 580 -AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSPPLEASSVNYESIKHE 638  
| | : : | : | | : : : | | : | | : | | :  
Db 372 PATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVVAEET 431

Qy 639 PENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEP 697  
| | | | : : : | : : | | : | | : | : : | |  
Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVSTPPTTASVPETTAPPA 491

Qy 698 P-----DFSDYSEMAKVEQVPDPHSEL-----VEDSSPDSEPVDLFSDDSI--DVPQK 744  
| | | | : | | | : | | : | | : | : |  
Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDL 550

Qy 745 QDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEV 804  
: | : : | : : : : | : : : : | : : : |  
Db 551 LEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603

Qy 805 STLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDFPTLI 860  
| : | | : : : : | | : | | | | | : |  
Db 604 SLATPTEPIPVEAPVVIQEAVIDAV-----EVPVTETST---SIP-ETTVEFPEAV 649

Qy 861 SSKTDSFSLKAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDL 906  
: | | : | : : : | | | | : : : :  
Db 650 AEKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701

Qy 907 KNIQPKVEEKISFSDDFSNGSATSQVLL---LP-----PDVSALG----- 944  
| | | : : : : : : : : : : : :  
Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760

Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLY 996  
: | | : | | : | | : : : | | : | : | |  
Db 761 ITAGDNPNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814

Qy 997 WRDIKKTGV 1005  
| | : : | |  
Db 815 -RDLQTTDV 822

RESULT 10  
A47283  
calphotin - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster  
 C;Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000  
 C;Accession: A47283  
 R;Ballinger, D.G.; Xue, N.; Harshman, K.D.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993  
 A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and contains a leucine zipper.  
 A;Reference number: A47283; MUID:93165730; PMID:8434015  
 A;Contents: photoreceptor cells  
 A;Accession: A47283  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-873 <BAL>  
 A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g157072  
 A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIIP:124959)  
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

Query Match 5.4%; Score 320.5; DB 2; Length 873;  
 Best Local Similarity 22.5%; Pred. No. 6e-06;  
 Matches 235; Conservative 122; Mismatches 367; Indels 321; Gaps 50;

```

Qy      59 PAAGLSAAPV-PTAPAAGAPLMDFGNDVFPAPRGPLPAAP----PVAPERQPSW-DPSP 112
      | :  ||| | :| ||  ::  | ||  | |||  |||  | :  |
Db      9 PVSAPVAAPVTPSAVAAPVQVVSPA AVAVAPVAPAPAAPTAVTPVAP--PPTLASVQP 66

Qy     113 VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPP-----A 163
      : ||||| :| :|| :| :|  ||  | ||  | || |||
Db     67 ATVTVPAPAPIAAASVAP---VASVAPPVVAAPTTPA-----ASPVSTPPVAVAQIPVAV 118

Qy     164 PAPAAPP----STPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQEDFPSVLLET-- 217
      || |||  || ||  ::|  | |
Db     119 SAPVAPPVAATPTPVAP-----IPVAAPVIATPPVAASAPT 154

Qy     218 -AASXPSLSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLT 276
      || | :|| :|  | :|  | | :  : | : : |
Db     155 PAAVTPVWSPVIAT-----PPVVPANTT----VPVAAPVAAPVAAVPVVPVLA 199

Qy     277 EFSELEYSEMGSFSVSPKAESAVIVAN-----PREEIIVKNKDEEEKLVSNILHXQQE 331
      :| :|  | :||  | || |
Db     200 P-----AVAPAV--APVVAETPAPPPVAEIPVAT----- 226

Qy     332 LPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDM 391
      :| :  | :| || :|  : | | | |  | | |
Db     227 IPECVAPLIPEVSVVAT---KPLAAAEPPVVAPPATET-----PVVAPAAASPH 272

Qy     392 LAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCA 451
      ::  :| : : :|  ||  :  : | :| |
Db     273 VSVAPAVETAVVAPVS-----ASTEPPV---AAATLTTA 303

Qy     452 PFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDS 511
      |  ||  | :| |  |||
Db     304 PETPAL-----APVVAESQ-----VAA--- 320

Qy     512 ETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEV 571
      |  |  | || :| :|  :| ||  :| ||  :| |
Db     321 -----NTVVATPPTPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPV 364

```

Qy 572 MQESLYPA-----AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSS 622  
 ||: || : : | : | || : : || : |  
 Db 365 AAESI-PAPVVATTPVPATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVL 423

Qy 623 SPLEASSVNYESIKHEPENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYIS 681  
 |: | : || | : : : | : | : | || : |  
 Db 424 PPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVS 483

Qy 682 IACDLIKETKLSAEPAP-----DFSDYSEMAKVEQPVPDHSEL-----VEDSSPDSEPV 730  
 : : || | | || | : || | : | : |  
 Db 484 TPPTTASVPETTAPPAAVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAE 542

Qy 731 DLFSDDSSIP--DVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788  
 || : | : | : : | : : | : ||  
 Db 543 DLIIEPVEPPAPIPDLLLEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEV 595

Qy 789 KLSLDNTKDTLLPDEVSTLSKKEKIPLQ---MEELSTAVYSNDDLFISKEAQIRETETF 844  
 : : : | | : | || : : | | | : || |  
 Db 596 AVAPITAPEPIPEPEPSLATPTEPIPVVEAPVVIQEAVDV-----EVPVTETST- 644

Qy 845 SDSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-- 901  
 | | | ||| : : | | : | : : : || || | || :  
 Db 645 --SIP-ETTVEFPEAVAQKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTP 693

Qy 902 -----HDLCLKNIQPKVEEKISFSDDFSKNGSATSQVLL----LP-----PDVS 941  
 | : : | | | : : : : : : : : : : | : ||  
 Db 694 AVEIVTAAAEVSDTAIPLIDPPVPQEIAVA-EIPETETKPAEVIVEQSTIPIEAPVPEVS 752

Qy 942 ALG-----HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSA 980  
 : | | : | | : | | : : : ||  
 Db 753 KYAEPVISEAPAAEVPITAGDNPNTSVGISEVV-PTIAEKPVVEVPTSEIPEQSSSPSD 811

Qy 981 IFSADLGKTSVVDLLYWRDIKKTGV 1005  
 | : | : || || : | |  
 Db 812 --SVPVAK--ITPLL--RDLQTTDV 830

# RESULT 11

T34418

hypothetical protein F12F3.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C;Accession: T34418

R;Fulton, B.; Wohldmann, P.

submitted to the EMBL Data Library, July 1998

A;Description: The sequence of *C. elegans* cosmid F12F3.

A;Reference number: Z21521

A;Accession: T34418

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3488 <FUL>

A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3

A;Experimental source: strain Bristol N2; clone F12F3

C;Genetics:

A;Gene: CESP:F12F3.3

A;Map position: 5



A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1

Query Match 5.1%; Score 299.5; DB 2; Length 3488;  
Best Local Similarity 20.6%; Pred. No. 0.0003;  
Matches 272; Conservative 187; Mismatches 475; Indels 387; Gaps 57;

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Qy      1 MEDLDQSPLV--SSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEV---- 54
          ::::| | ::      | : :| | : ::| | | :      | | : : |::|
Db      340 VDEVDDSTVLEEKKDDGDDKSKPKTKKKIIKKKETPESEQVTAAEPEQQKISEVDVQSV 399

Qy      55 -----LERKPAA-----GLSAAPVPT-----APAAGA-----PLMD-----FGNDF 85
          :|| |      || | :      | |      | |      | |
Db      400 ETEVGAKKKPDAEKPTDLSKAKKDSKSKKSDEPEASTEESTTEKPTNDKTSKKSAAEKK 459

Qy      86 VPPAPR---GPLPAAPPVAPERQPSWDPSPVSVSTVPA-----PSPLSAAAV 128
          | |      || | || : : | |      | : |      | : |
Db      460 VKPKKEVTGKPLEAKKPVEDKKDASQPSSSKESPPTDGKKKKQIPKALFIPDEISSRFG 519

Qy     129 SPSKL-----PEDDEPPARPP--PPPPASVS-----PQAEPVWTPPPAP 164
          || :      :      | : | | |||      :|| : :
Db     520 DPSTMHSETNITTTIRGREGSADAKTPLVEPLSASVSMKVFTLVESAKEAEFSFKRRSE 579

Qy     165 AP-----AAPPSTPAAPK-----RRGSSGAVVXXXXKIMD----LKEQPGN----- 201
          |      ||: : |      : | : |:: : | : |      :|| :
Db     580 TPDDKSRKKEGLPPAKKSEKKDEVTAEQSTEALIESKKKEVDESKISEQQPSDKNKSEV 639

Qy     202 ----TISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGNLSTVL---PTEGTLQEN 254
          :|| |      |      | :      : | :      : | ||      : : ::
Db     640 VGVPEKAAGPETKKDV--SEIEEVPKKKTIKKKTEKSDSSISQKSNVLKPADDDKSKSD 697

Qy     255 VSEASKEVSEKAKTLLID-----RDLTEFSELE-----YSEMGSSFSVSP 294
          |:: ||: :| :      |      | | : | |      :| || :|
Db     698 VTDKSKKTTEDQTKVATDSKLEKAADTTKQIETETVVDDKSKKKVLKKKTEKSDSF-ISQ 756

Qy     295 KAESAVIV--ANPRE----EIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKED----- 343
          |:: : :| | :      :| || ::|| : :| : :| | : |
Db     757 KSETPPVVEPTKPAESEAQKIAEVNKAKKQKEVDDNL---KREA EVAAKKIAD EKLKIEA 813

Qy     344 -----EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG 395
          || ::|| | : : : : | : : | : :| : | |
Db     814 EANIKKTAEEVAAKKQKEKDEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEAD---AVK 870

Qy     396 GKIESNLESKVD--KKCFAD--SLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCA 451
          : | | ::||: || || ||: : | : | : | | : ||
Db     871 KQKELNEKNKLEAAKKSAAADKLKLEESAAKSKKVSEESVKF---GEEKTKAGEKTVQV 927

Qy     452 PFNPAATESIATNIFPLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDS 511
          | : ::| |      | | | | :||| :|| ||| : | : |
Db     928 ESEPTSKKTIDTKDVGATE-PADE--TPKKKI I KKK----TEKSDSS-----ISQKS 972

Qy     512 ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTK-----IAYETKMDL 565
          || : : :| | :      | : || :| : : | |      || :|| :
Db     973 ATD---SEKVSQKEQDEPTKPAVSETQMVT EADKSKKQKETDEKLKLD AEIAAKTKQEA 1029

Qy     566 VQTSEV-MQESLYPAAQLCPSFEESEATPSPVLDP-IVMEAPLNSAVPSAGASVIQPSSS 623
          : |:: || : :      | : | | : :| : : : | | : : :
Db    1030 DEKSKLDAQEKIKKVS-----EDDAARKEKELNDKLKLESEIATKKASADKLKLEEQAQ 1083
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A;Residues: 1-3924 <CHA>  
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
 R;Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.  
 J. Cell Biol. 114, 241-253, 1991  
 A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins  
 reveal a family of alternatively spliced genes.  
 A;Reference number: A39643; MUID:91302466; PMID:1830053  
 A;Accession: A39643  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-2077 <OT1>  
 A;Cross-references: GB:X56957  
 A;Accession: B39643  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-1443,3585-3924 <OTT>  
 A;Cross-references: EMBL:X56958  
 R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux,  
 S.E.; Ward, D.C.; Forget, B.G.  
 Genomics 10, 858-866, 1991  
 A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin  
 gene.  
 A;Reference number: A40334; MUID:92009921; PMID:1833308  
 A;Accession: A40334  
 A;Molecule type: DNA  
 A;Residues: 463-474,'PE',477-495 <TSE>  
 A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648  
 R;Chan, W.; Kordeli, E.; Bennett, V.  
 J. Cell Biol. 123, 1463-1473, 1993  
 A;Title: 440-kD ankyrinB: structure of the major developmentally regulated  
 domain and selective localization in unmyelinated axons.  
 A;Reference number: A49462; MUID:94075409; PMID:8253844  
 A;Accession: A49462  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-3924 <RES>  
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
 C;Genetics:  
 A;Gene: GDB:ANK2  
 A;Cross-references: GDB:127607; OMIM:106410  
 A;Map position: 4q25-4q27  
 C;Superfamily: ankyrin; ankyrin repeat homology  
 C;Keywords: alternative splicing  
 F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>  
 F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>  
 F;63-95/Domain: ankyrin repeat homology <AN01>  
 F;96-128/Domain: ankyrin repeat homology <AN02>  
 F;129-161/Domain: ankyrin repeat homology <AN03>  
 F;162-190/Domain: ankyrin repeat homology <AN04>  
 F;191-223/Domain: ankyrin repeat homology <AN05>  
 F;232-264/Domain: ankyrin repeat homology <AN06>  
 F;265-297/Domain: ankyrin repeat homology <AN07>  
 F;298-330/Domain: ankyrin repeat homology <AN08>  
 F;331-363/Domain: ankyrin repeat homology <AN09>  
 F;364-396/Domain: ankyrin repeat homology <AN10>  
 F;397-429/Domain: ankyrin repeat homology <AN11>  
 F;430-462/Domain: ankyrin repeat homology <AN12>

F;463-495/Domain: ankyrin repeat homology <AN13>  
 F;496-528/Domain: ankyrin repeat homology <AN14>  
 F;529-561/Domain: ankyrin repeat homology <AN15>  
 F;562-594/Domain: ankyrin repeat homology <AN16>  
 F;595-627/Domain: ankyrin repeat homology <AN17>  
 F;628-660/Domain: ankyrin repeat homology <AN18>  
 F;661-693/Domain: ankyrin repeat homology <AN19>  
 F;694-726/Domain: ankyrin repeat homology <AN20>  
 F;727-759/Domain: ankyrin repeat homology <AN21>  
 F;760-792/Domain: ankyrin repeat homology <AN22>  
 F;793-825/Domain: ankyrin repeat homology <AN23>

Query Match 5.0%; Score 299; DB 2; Length 3924;  
 Best Local Similarity 21.5%; Pred. No. 0.00037;  
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

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Qy      14 DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK 58
      | ||      :|      |      | : :::::| | :      | |      | |
Db      1648 DIPDETQSTQKQHKPSLGIKKPVRRLKEKQKQKEEGLQASAEKAELKKGSSEESLGED 1707

Qy      59 PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----- 92
      | ||: |:|| | :||::      | :| :|
Db      1708 P--GLAPEPLPTVKAT--SPLIEETPIGSIKDKVKALQKRVEDEQKGRSKLPPIRVKGKEDV 1764

Qy      93 -----PLPAA-PPVAPERQPSWDPSP-----VSSTVPAPSPL 123
      | ||| | : ||      ||      ||      || :||
Db      1765 PKKTTHRPHPAASPSLKSERHAPGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV 1824

Qy     124 SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW 159
      | :|      |||| | | :      | || | : : ||
Db     1825 SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSTKTERHPPVSPSGKTDKRPPV- 1883

Qy     160 TPPAPAPAAPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPNGTISAGQEDFPSVLLE 216
      :|      || :| : :|      ||      | || :| : : |
Db     1884 SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLVPVSPSG 1934

Qy     217 TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT 268
      | :|| | :| : | :      : | | : | | : || |
Db     1935 KTEKQPPVSPTS KTERIEETMSVRELMKAFQSGQDPSKHKTGLFEHKSQKQKQPEKGKV 1994

Qy     269 -----LLIDRDLTEFSELEYSEMGSFSVSPKAES--AVIVANPREEIIVKNKDE-- 316
      :| | : : :| : : | | : ||| | | : : | || :|
Db     1995 RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAESKRGVRVSS----IGVKKEDAAG 2049

Qy     317 -EEKLVSNNI-----LHXQQELPTALTCLKVKE-----DEVV 346
      :||::| : | : | :| | : | | : | | : ||:
Db     2050 GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGMDLQISPDRKTSTDFSEVI 2107

Qy     347 SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED----- 388
      | : | : : | : | : : | || : : | : :
Db     2108 KQELEDNDKYQQFRLSEETEKALHLQVLTSPFNTTFPLDYMKDEFLPALSLQSGALDG 2167

Qy     389 -SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDSSESNDDTSFPSTPEGIKDRS 444
      | : | | | : : | | | : | : | | : | : : : :
Db     2168 SSES LKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT 2225

Qy     445 GAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPF 504

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      |           :           | |           | |::: |           | | : | : : | |::
Db      2226 G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTEDSETSTESFQKE 2277

Qy      505 FVAAQDSETDYVTTDNLTKVTEEVVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKM 563
      :|           |: |           :| | | |           :| |           |: |::|
Db      2278 ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT---EEAACDEGQRTFGSS-AHKT-- 2330

Qy      564 DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVL-----PDIVMEAP--LNSAV 610
      ||           ||           : :::| | |           | | : | | | |
Db      2331 ---QTDSEAQES-----TATSDETKALPLPEASVKTDGTESKPQGVIRSPQGLELAL 2380

Qy      611 PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVSG 657
      || : | :           | | | | | : : | : | : | | : | | : |
Db      2381 PSRDSEVL SAVADDSLAVSHKDSLEASPVLEDNSSHKTPDSLEPSPLKESPCRDSLESSP 2440

Qy      658 IKEEIKE---PEN--INAALQETE--APYISACDLIKETKLSAEPAPDFSDYSEMAKVE 710
      : : : | | : : | : | : | | | : | : : | | | : | : |
Db      2441 VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE 2490

Qy      711 QPVPDHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI 765
      | : | : | | | : : | : | : | : | : |
Db      2491 Q-----TSLMESSGKSPLSPDTPSSEEVSYEVTPKTTDVSTPKPAVIHECAEED----- 2539

Qy      766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK----EKIPLQMEELS 821
      : | | | | | | | | | : | | : | : : | : | | | |
Db      2540 DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAQKRDYKKEPKQEESSS 2589

Qy      822 TAVYSNDDLFISKEA-QIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVS 880
      : | : | | : : | : | : | : | : | : | : | :
Db      2590 S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSESRKVSSSSSES----- 2633

Qy      881 HKSEIANAPDGAGS-----LPCTELPHDL SLKN-----IQPKVEEKISF--SDD 922
      : | : | | | | | : | | : : | | | : : : | : |
Db      2634 -EPELAQLKKGADSGLLPEPVIRVQPPSPLPSSMDSNSSPEEVQFQPVVSKQYTFKM NED 2692

Qy      923 FSKNGSATS KVL L LPPDV SALGHTQAEIESIVKPKVLEKEAEKKLP SD-----TEKEDRS 977
      : : : | : : | | | | | | |
Db      2693 TQEEP GKSEE-----EKDSESHLAEDRHAVSTEAE DRS 2725

```

# RESULT 13

T16251

hypothetical protein F35A5.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000

C;Accession: T16251

R;Leimbach, D.

submitted to the EMBL Data Library, January 1996

A;Description: The sequence of *C. elegans* cosmid F35A5.

A;Reference number: Z18485

A;Accession: T16251

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1274 <LEI>

A;Cross-references: EMBL:U46675; NID:g1166613; PID:g1166621; PIDN:AAB52641.1;

GSPDB:GN00028; CESP:F35A5.1

A;Experimental source: strain Bristol N2; clone F35A5

C;Genetics:  
A;Gene: CESP:F35A5.1  
A;Map position: X  
A;Introns: 1272/2

Query Match 4.9%; Score 290.5; DB 2; Length 1274;  
Best Local Similarity 20.5%; Pred. No. 0.00017;  
Matches 221; Conservative 126; Mismatches 417; Indels 313; Gaps 45;

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Qy      13 SDSPPRP--QPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPT 70
      | :|| | || |: | |||| | ||: ||: ||: ||
Db      2 SRAPPTPIKNPAKKWKPPWESVDEEEEME-----VDEETPAPSKLEKKPSLKRKDAPTKP 56

Qy     71 APAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSP 130
      |: ||| | :| || : | | |: || |
Db     57 VSPSGAP-----SPVFIKNPVKKWKAPWEDDEPMEEAPAAP-----VP 94

Qy    131 SKLPEDDEP---PARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVX 187
      :| | | ||: | | : : | || || || :
Db     95 AKKVRDPSPKKVPAPKPRDASPKKIMAAKK----EPETLPAVPP-TPVKNPVKKFKAPWED 149

Qy    188 XXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP-SLSPLSAASFKEHEYLGNLSTVLP 246
      : |:|: | |: | : ||: | || || |||: : | |
Db    150 DEVDVDVKDAP--TVPAKKTPVLKKKEPAAAAKPRDPSPKKAAPSKEHDPI-----VPP 202

Qy    247 TEGTLQENVSEASKEVSEKAKTLLIDRDL--TEFSELE-----YSEMGSFSVSPKA 296
      | | :| | | :| | | | : | || | :
Db    203 T-----PIKNPAKKWKPPWEDDEVPTTEEIKEPEPATRKVPALKKKEPSTSVKPV 252

Qy    297 ESAVIVANPREEIIVKNKDE-----EEKLVSNNILHXQQELPTALT 339
      : : :| :| | :| | :| : : :| :
Db    253 D-----PSPTKKVPVKKEPEVPPTPIKNPTKKWKPPWEDETPVEEV--KEPPVPEKKAPV 305

Qy    340 VKEDVVSSEKAKDSFNEKR-----VAVEAPMREEYADFKPFERVWEVKDSKEDS 389
      :|: : : ||: | | | :| : || || | :
Db    306 LKKKDPAPAAKARDPSPSKAAPKKVEPSSPVVPPTPVKNPVKKYKP---PWEVDDEPAE- 361

Qy    390 DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYIT 449
      | | | :|| |: | | : : | | :| | :
Db    362 -----EVKKPSAPEKK--TPVLKRKEPEPSSTPSSDPSPKKAAPAVKPRDSSPKK 410

Qy    450 CAPF--NPAATESIATNIFLLEDPTSE-----NXTDEKKIEE-KKAQIVTEKNTSTKTS 501
      | :| | | | : :| : || :|| |: : | |
Db    411 ATPLQADPKAQEVPTPV----KNPVKKYKPPWEVDDEDVVEEVKQPEAPAKKTPVLKRK 466

Qy    502 NPFFVAAQDSETDYVTNDLTKVTEEVVANMPE-----GLTPDLVQ---- 542
      | ||: | | | | || | || |
Db    467 EP---AAKD-----TAKPATSKTPET----PEKKDPVKPRDSSPKKVAAPKPSAQAPAT 513

Qy    543 -----EACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEES 589
      | | : :|: | :| : :|| | | :
Db    514 PVKNPVKKWRPPWEDDETADDVSKPTDAKKTPSLAKKDPAPAKESLKPADTKAPAKPR 573

Qy    590 EATPSPVLPDIVMEAPLSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAM 649
      : :| | | | : | | | | :| :| | :
Db    574 DSPKKVAP-----TAPEKKTPLAKKEPAGPADSKTKEPEKSKPRDPSPKKAVP 623
```

Qy 650 S-----VSLKVSIGK--EEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD 702  
 : : : : | | : : : | : : : | : :  
 Db 624 AKPVPKTEVAPAAVKKPEPISKPKDTAPKKAEPNSPVV-----PPTP---- 665

Qy 703 YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFE 762  
 | : | | | : : : | : : : | : : : | : :  
 Db 666 -----VKNPVKKWKPPWEDDDAPAKPVSL-----PEPEKKTPLAKKAPTKPDSE 710

Qy 763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822  
 : | | |  
 Db 711 -----AAADPVSGP----- 719

Qy 823 AVYSNDDLFISKEAQIRETETFSDDSPIEII-----DEFPTLISSKTDSEFSKLAREYT 875  
 | : | : : : | : : : | : : : | : : : | : : :  
 Db 720 ---SSKDPKLAKKAPVKP---RDPSPMKAVPIKPAKTEVPPAVVKKPEPVAK----- 766

Qy 876 DLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE-----EKISFSDDFSKNGSA 929  
 : | | | : : : | : : : | : : : | : : : | : : :  
 Db 767 SRDPSPKK--AKAEPNSPVVPPT--PVKNPVKKWKPPWEDDDAPAEVNVPEPEKKTPL 822

Qy 930 TSKVLLLPPDVS-----ALGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSP 978  
 | : | | | | : : : | : : : | : : : | : : :  
 Db 823 AKKTPVKPRDPSPKKAVPAKPKSTKTDAAPPVSVKKPEPVSKPKE---PSPKKAEPNSP 876

# RESULT 14

A56577

microtubule-associated protein MAP 1B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997

C;Accession: A56577

R;Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.

Eur. J. Cell Biol. 57, 66-74, 1992

A;Title: Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.

A;Reference number: A56577; MUID:92347374; PMID:1639092

A;Accession: A56577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2364 <ZAU>

A;Cross-references: GB:X60550

A;Experimental source: brain

A;Note: nucleotide sequence not given; conceptual translation not complete

C;Superfamily: microtubule-associated protein MAP1B

Query Match 4.9%; Score 289; DB 2; Length 2364;

Best Local Similarity 20.9%; Pred. No. 0.00047;

Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

Qy 30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDVFPPA 89  
 | | ||| ||| : : : | : : | | | | : ||:  
 Db 909 EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYMAVVDKAAEAGVTEQY--DFL--- 963

Qy 90 PRGPLPAAPP--VAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP 147  
 || | : | : : | : | | | : | |  
 Db 964 ---GTPAKQPGVQSPSREPA---SSIHDETLPGGSESEATA-----SDEENREDQPEEF 1011

Qy 148 PASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ 207  
|: : | | || | : | : | | |  
Db 1012 TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNEETESPSQ 1055

Qy 208 E-----DFPSVLLETAASXP---SLSPLSAASFKE---HEYLGNLSTVLPTEGTLQENV 255  
| : | | | : | | : : | : | : | :  
Db 1056 EFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEEDKF 1115

Qy 256 SEAS-----KEVSEK-----AKTLLIDRDLTE 277  
|::: |::: | | : | :  
Db 1116 SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPSPIEKTPLGERSV-N 1174

Qy 278 FS----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIVKNK----- 314  
|| | : | | : : || | | : | | | : : :  
Db 1175 FSLTPNEIKASAEGEATAVVSPGVTQAVVEEHCASPEEKTLEVVSQSVTGSAGHTPY 1234

Qy 315 ----DEEEKLVSNILHXQQELPTALTCLVKEDEVVSSE--KAKDSFNEKRVAVEAPMRE 368  
||: : : | : | | | : || | | : : || |  
Db 1235 QSPTDEKSSHLPTTEVTEAQAQVP-----VSFEFTEAKDE-NER--SSISPMDE 1279

Qy 369 EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDKKCFADSL 415  
| : | | : : : : | | : | | | | : | : |  
Db 1280 PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRSESPFEGKNGKQGFSD-- 1337

Qy 416 EQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNP---AATESIATNIFPLLED- 471  
| : | | | | : : | : | | : | : | : | |  
Db 1338 -----KESPVS-DLTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE 1390

Qy 472 -----PTSENXTDEKKIEEKKAIQVTEKNTSTKTSNPFVAAQDSETDYVTTDNLT 523  
|| : : : | : | | : | | : | : | : :  
Db 1391 RKLGGDGSPTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS 1447

Qy 524 VTEEVVA--NMPEGLTPDLVQEACESELNEVTGKTIAYETKMDLVQTSEVMQES-LYPAA 580  
| : || : || | | : : | : | : : || | | : : | :  
Db 1448 VSTASVATSSFPPTDD-VSPSLHAEVGSHPHSTEVDSDLVSVVQTPTTFQETEMSPSK 1506

Qy 581 QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P 611  
: || : : : | : : | : | : |  
Db 1507 EECPRMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRSQSPDHP 1566

Qy 612 SAGASVIQ----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG 657  
: || : : | : | : | : | | | : || : : |  
Db 1567 TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPPTTEPSYTDNDLSELISVSQVEASP 1626

Qy 658 IKEEIKEPENINAALQETE-----APYISIACDLIKE---TKLSAEP----- 696  
| | : || | : | | : : | | :  
Db 1627 STSSAHTPSQIASPLQEDTLSDVPPRDMSLYASLASEKVQSLGEKLSPKSDISPLTPR 1686

Qy 697 -----APDFSDYSEMAK-----VEQVPDPHSELVEDS----- 723  
: | || : | | : | | : : | :  
Db 1687 ESSPTYSPGFSSTSGAKESTAAYQTSSSPIDAAAAEPYGRSSMLFDTMQHHLALSRLD 1746

Qy 724 -----SPDSEPVDLFSDD---SIPDVP---QKQD 746  
|| | | | : | | : | :  
Db 1747 LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYYEYKTE 1806

Qy 747 ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD 797



```

      | :      | | : | :      | | : | | | | : : :
Db      1807 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTTRTPEEGGYSY-----EISEK 1858

Qy      798 TLLPDEVs--TLskKEKIPLQMEELSTAVYSNDD-----LFISKEA 836
      | | | | | : | | : : : | : | : | :
Db      1859 TTRTPEVSGYTYEKTERRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 1918

Qy      837 QIRETETFSdSSP-----IEIIDEFPTLISSKTDSFskLAREYT-----DL 877
      | | | : | | | : : : | : | : | | | |
Db      1919 YSYETTTKTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 1978

Qy      878 -----EVSH-KSEIANA---PDG-----AGSLPCTELPHDLsLKNIQP-----KV 913
      | | | : : : | : | | | | : | :
Db      1979 CLVSSCEfKHPKTELSPSFINPNPLEWFAGEEPTeesERPLTQSGGAPPPSGGKQQGRQC 2038

Qy      914 EEKISfSDDfSKNGSATSkvLLLLPPDVsalGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970
      : | | | | | | | : | | | : | | : : |
Db      2039 DETPPTSVSESAPSQTDSdv---PPETE-----ECPSITADANLDSEDESEtiPTDKT 2088

Qy      971 -----TEKEDRSPS-----AIFsADLGKTSVVDLLYWRDIKKTG 1004
      : | | | | | : | | | | | |
Db      2089 VTYKHMDPPPAPMQDRSPSPRHDPVSMVDPEALAIeqNLGKALKKDLKEKAKTKKPG 2145

```

# RESULT 15

## QRMSP1

microtubule-associated protein MAP1B - mouse

N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein MAP1.2; microtubule-associated protein MAP5

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 01-Sep-2000

C;Accession: S07549; S44387; A33645

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2 and tau.

A;Reference number: A33645; MUID:90094539; PMID:2480963

A;Accession: S07549

A;Molecule type: mRNA

A;Residues: 1-2464 <NOB>

A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000

R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.

Arch. Biochem. Biophys. 310, 428-432, 1994

A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A;Reference number: S44387; MUID:94234720; PMID:8179328

A;Accession: S44387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 653-663,'IC' <SAN>

C;Superfamily: microtubule-associated protein MAP1B

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <MTB>

F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-694,695-698,699-702,708-711,712-715,716-719,720-723,727-730,758-761,764-767,783-786/Region: 4-residue repeats (K/R-K-E/D-X)

F;1861-2064/Region: 17-residue repeats

F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (covalent) #status predicted  
 F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 289; DB 1; Length 2464;  
 Best Local Similarity 19.8%; Pred. No. 0.0005;  
 Matches 262; Conservative 148; Mismatches 474; Indels 442; Gaps 55;

Qy	32	EDEEEEEEEEEDEDEDL-EELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAP	90
		:        :       ::         :	
Db	1009	EAEQSEEEGEEEDKAEDAREEGYEPDKTEADYVMAVADKAAEAGVTEEQYGY-----	1061
Qy	91	RGPLPAAPPV-APERQPSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPA	149
		: :   : :   :        :	
Db	1062	LGTSAKQPGIQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTA	1112
Qy	150	SVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED	209
		: :         :  :	
Db	1113	TSGYTQSTIEISSEPTPMDEMSTP-----RDVMSDETNNNEETESPSQEF	1156
Qy	210	FPSVLLETAASXPSLSPLSAASFK-----EHEYLGNLSTVLPTEGTLQENVSE	257
		::   :     :  :   :   : :  :	
Db	1157	VNITKYESSLYSQEYSKPAVASFNGLSEGSKTDATDGKDYNASASTISPPSSMEEDKFSK	1216
Qy	258	AS-----KEVSEK-----AKTLLIDRDLTEFS	279
		:: : :::      :  :	
Db	1217	SALRDAYCSEEKELKASAELDIKDVSDERLSPAKSPSLSPSPSPSPPIEKTPLGERSV-NFS	1275
Qy	280	----ELEYSEMGSFSVSPKAESAVI---VANPRE---EIIVKNK-----	314
		::     :        :   :     :: ::	
Db	1276	LTPNEIKVSAEGEARSVSPGVQTQAVVEEHCASPEEKTLEVVSQSQSVTGSAGHTPYQSP	1335
Qy	315	-DEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADF	373
		: : :   :  : :      :   :	
Db	1336	TDEKSSHLPTEVSENAQAVPVSF-----EFSEAKDE-NER--ASLSPMDEFPVPDS	1382
Qy	374	K-PFERVWE-----VKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE	425
		:    :  :    :    :	
Db	1383	ESPVEKVLSPLRSPPLLGSSEPYEDFLSADSKVLGR-----RSESPFE	1425
Qy	426	SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXT-----	478
		:   :    :    :	
Db	1426	GKNGKQGFPDRESPVSD-----LTSTGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS	1480
Qy	479	-----DEKKI-----EKKKAQIVTEKNTSTKTSNPFVAAQDSETD	514
		::: :  :      ::     :	
Db	1481	SQSALALDERKLGGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDT	1538
Qy	515	YVTTDNLTKVTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVM	572
		: :  :    :        : : :  :: : :	
Db	1539	YSHMEGVASVSTASVATSSSFPEPTTDD-VSPSLHAEVGSHPHSTEVDSDLVSVVQTPTTF	1597
Qy	573	QES-LYPAAQLCP-----SFESEATPSPVLPDIVMEAPLNSAV--	610
		: :  : :    : :   : :   :  :	
Db	1598	QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD	1657

Qy 611 -----PSAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAM 649  
 | : | | | : | : : | : | : | :  
 Db 1658 FSRQSPDHPTLGASVLHITENGPTTEVDYSPCDIQDSSLSHKIPPTTEEPSYTQDNDLSELI 1717

Qy 650 SVS-LKVSGIKEEIKEPENINAALQETE-----APYISIACDLIKE---TKLSAE 695  
 | | | : : | | : | | : | : | : | : | :  
 Db 1718 SVSQVEASPSTSSAHTPSQIASPLQEDTLSDVVPREMSLYASLASEKVQSLEGEKLSPK 1777

Qy 696 P-----APDFSDYSEMAK-----VEQPVPDHSELVEDS- 723  
 : | | | : | : | : | : | : | :  
 Db 1778 SDISPLTPRESSPLYSPGFS DSTSAAKETAAAHQASSSPPIDAATAEPYGRSSMLFDTM 1837

Qy 724 -----SPDSEPVDLFSD-----DS 737  
 | | | | | | | | | |  
 Db 1838 QHHLALNRDLTTSSVEKDSGGKTPGDFNYAYQKPENAAAGSPDEEDYDYESQEKTIIRTHDV 1897

Qy 738 IPDVPQKQDETVMML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788  
 : : : | : | : | : | : | : | : | :  
 Db 1898 VRYYYEKTERTIKSPCDSGYSYETIEKTTKTPEDGGYTCEITEKTRTPEEGGYSY---- 1953

Qy 789 KLSLDNTKDTLLPDEVSS--TLSKKEKIPLQMEELSTAVYSNDD----- 829  
 : : : | | | | | : : : : | :  
 Db 1954 ----EISEKTTRTPEVSGYTYEKTERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEK 2009

Qy 830 --LFISKEAQIRETETFS DSSP-----IEIIDEFPTLISSKTDSFSKLAREYT----- 875  
 | | : | | : | | | : : : | : | : | |  
 Db 2010 ITSFPESSESYSYETSTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTTEKKSP 2069

Qy 876 -----DL-----EVSH-KSEIANA---PDG----AGSLPCTELPHDL SLKNIQP--- 911  
 | | | | | : : : : | : | | | : | :  
 Db 2070 SEARQDVDLCLVSSCEFKHPKTELSPSFINPNLEWFAGEEPTEESEKPLTQSGGAPPPS 2129

Qy 912 -----KVEEKISFSDDFS KNKSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAE 964  
 : : | | | | | | : | | : : | |  
 Db 2130 GKGQQGRQCDETPPTSVSESAPSQTDS DV---PPETE-----ECPSITADANIDSEDE 2179

Qy 965 KK-LPSD-----TEKEDRSPS-----AIFSADLGKTSVVDLLYWR 998  
 : : : | : | | | : | | | | |  
 Db 2180 SETIPTDKTVTYKHMDPPPAPMQDRSPSPRHPDVMVDPDALAVDQNLGKAVKKDLKEKT 2239

Qy 999 DIKKTG 1004  
 | | |  
 Db 2240 KTKKPG 2245

Search completed: September 3, 2004, 16:09:59  
 Job time : 38.1547 secs

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:09:02 ; Search time 116.281 Seconds  
(without alignments)  
3191.803 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	

1	5815	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
2	5815	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
3	5815	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
4	5810	98.1	1192	9	US-09-789-386-2	Sequence 2, Appli
5	5810	98.1	1192	9	US-09-893-348-23	Sequence 23, Appl
6	5810	98.1	1192	12	US-10-267-502-429	Sequence 429, App
7	5810	98.1	1192	16	US-10-327-213-9	Sequence 9, Appli
8	5810	98.1	1192	16	US-10-466-258-9	Sequence 9, Appli
9	5794	97.8	1192	12	US-10-408-967-7	Sequence 7, Appli
10	4296.5	72.5	1163	9	US-09-893-348-18	Sequence 18, Appl
11	4277.5	72.2	1163	12	US-10-267-502-431	Sequence 431, App
12	1495.5	25.2	373	9	US-09-789-386-6	Sequence 6, Appli
13	1495.5	25.2	373	9	US-09-765-205-6	Sequence 6, Appli
14	1495.5	25.2	373	9	US-09-893-348-24	Sequence 24, Appl
15	1495.5	25.2	373	12	US-10-408-967-8	Sequence 8, Appli
16	1495.5	25.2	373	14	US-10-060-036-72	Sequence 72, Appl
17	1487.5	25.1	373	16	US-10-466-258-4	Sequence 4, Appli
18	1417	23.9	289	9	US-09-789-386-4	Sequence 4, Appli
19	1225.5	20.7	379	14	US-10-205-194-164	Sequence 164, App
20	1187	20.0	360	9	US-09-893-348-20	Sequence 20, Appl
21	931	15.7	199	9	US-09-893-348-25	Sequence 25, Appl
22	931	15.7	199	12	US-10-660-946-1	Sequence 1, Appli
23	924	15.6	199	12	US-10-408-967-9	Sequence 9, Appli
24	922	15.6	199	12	US-09-978-360A-467	Sequence 467, App
25	908	15.3	199	9	US-09-893-348-21	Sequence 21, Appl
26	890	15.0	199	16	US-10-466-258-11	Sequence 11, Appl
27	791	13.4	777	14	US-10-205-219-93	Sequence 93, Appl
28	787.5	13.3	776	12	US-10-660-946-5	Sequence 5, Appli
29	787.5	13.3	776	12	US-10-267-502-430	Sequence 430, App
30	779	13.2	780	12	US-10-267-502-432	Sequence 432, App
31	705	11.9	356	12	US-10-660-946-6	Sequence 6, Appli
32	704	11.9	593	15	US-10-108-260A-2892	Sequence 2892, Ap
33	688	11.6	208	12	US-10-660-946-7	Sequence 7, Appli
34	671	11.3	267	12	US-10-660-946-8	Sequence 8, Appli
35	671	11.3	267	14	US-10-205-194-127	Sequence 127, App
36	630	10.6	266	12	US-10-276-774-2330	Sequence 2330, Ap
37	625.5	10.6	236	9	US-09-729-674-20	Sequence 20, Appl
38	625.5	10.6	236	9	US-09-765-205-26	Sequence 26, Appl
39	625.5	10.6	236	12	US-10-408-967-2	Sequence 2, Appli
40	625.5	10.6	269	14	US-10-106-698-6222	Sequence 6222, Ap
41	541.5	9.1	168	10	US-09-809-391-563	Sequence 563, App
42	541.5	9.1	168	10	US-09-882-171-563	Sequence 563, App
43	541.5	9.1	168	12	US-10-164-861-563	Sequence 563, App
44	520	8.8	222	12	US-10-267-502-428	Sequence 428, App
45	513	8.7	241	12	US-10-660-946-3	Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.



Db 481 PLLGDPTSENKTDEKKIEEKKAIQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE 540

Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586  
 |||

Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646  
 |||

Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660

Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE 705  
 |||

Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE 720

Qy 706 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQVDPQKQDETVMVLKESLTETSFESMI 765  
 |||

Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQVDPQKQDETVMVLKESLTETSFESMI 780

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 |||

Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 |||

Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPPDVSAALGH 945  
 |||

Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPPDVSAALGH 959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV 1005  
 |||

Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065  
 |||

Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1125  
 |||

Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1139

Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
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Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 2

US-09-972-599A-6

; Sequence 6, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06





QY 527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586  
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 Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600  
 |||  
 QY 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646  
 |||  
 Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660  
 |||  
 QY 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705  
 |||  
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720  
 |||  
 QY 706 MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIDPVPQKQDETVMVLKESLTETSFESMI 765  
 |||  
 Db 721 MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIDPVPQKQDETVMVLKESLTETSFESMI 780  
 |||  
 QY 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 |||  
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840  
 |||  
 QY 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 |||  
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900  
 |||  
 QY 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAALGH 945  
 |||  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSAALGH- 959  
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 QY 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAIDLKTSVVDLLYWRDIKKTGV 1005  
 |||  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019  
 |||  
 QY 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065  
 |||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079  
 |||  
 QY 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125  
 |||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139  
 |||  
 QY 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192  
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RESULT 3

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
 ; FILE REFERENCE: 210121.566  
 ; CURRENT APPLICATION NUMBER: US/10/060,036  
 ; CURRENT FILING DATE: 2002-01-30  
 ; NUMBER OF SEQ ID NOS: 4560  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 71  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-060-036-71

Query Match 98.2%; Score 5815; DB 14; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 5.8e-284;  
 Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF	600

Qy	587	EESEATPSVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFISKEAQIRETETFSDDSSPIEIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFISKEAQIRETETFSDDSSPIEIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSALSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 4

US-09-789-386-2

; Sequence 2, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30165-C1

; CURRENT APPLICATION NUMBER: US/09/789,386

; CURRENT FILING DATE: 2001-02-21

; PRIOR APPLICATION NUMBER: U.K. 9916898.1

; PRIOR FILING DATE: 1999-07-19

; PRIOR APPLICATION NUMBER: U.K. 9816024.5

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: US 09/359,208

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; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2
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Query Match          98.1%; Score 5810; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 1e-283;
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;
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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180

QY    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:          |:          : ||||||||||||||||||||||||||||
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

QY    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

QY    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV 346
      |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV 360

QY    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

QY    407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    421 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

QY    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 526
      ||| ||||| |||||||||||||||||||||||||||| ||||||||||||||||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 540

QY    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

QY    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
      |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660
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Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLP SDTEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

# RESULT 5

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

## ; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

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; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23
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Query Match          98.1%; Score 5810; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 1e-283;
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;
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QY      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120

QY    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
      |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180

QY    181 SSGA-----VVXXXXKIMDLKEQPNGNTISAGQEDFPSVLLETAASXPSLSP 226
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Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPNGNTISAGQEDFPSVLLETAASLPSLSP 240

QY    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
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Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

QY    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV 346
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Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV 360

QY    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

QY    407 DKKCFADSLEQTNHEKDSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      |||
Db    421 DKKCFADSLEQTNHEKDSESSNDDTSFSPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

QY    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE 526
      |||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540

QY    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      |||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

QY    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
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Db 601 E ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS SSPLEASSVNYESIKHEPENPPPYE 660  
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFSDYSE 705  
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFSDYSE 720  
 Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDD SIPDVPQKQDETVM LVKESLTETSFESMI 765  
 Db 721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDD SIPDVPQKQDETVM LVKESLTETSFESMI 780  
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840  
 Qy 826 SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 Db 841 SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900  
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLPPDV SALGH 945  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLPPDV SALA- 959  
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF S ADLGKTSVVDLLYWRDIKKTGV 1005  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIF S AELSKTSVVDLLYWRDIKKTGV 1019  
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I QAIQKSDEGHPFRAYLES 1065  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I QAIQKSDEGHPFRAYLES 1079  
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYV GALFNGLT 1125  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYV GALFNGLT 1139  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1192

RESULT 6

US-10-267-502-429

; Sequence 429, Application US/10267502

; Publication No. US20040071700A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Jaeseob

; APPLICANT: Galant, Ron

; TITLE OF INVENTION: Obesity Linked Genes

; FILE REFERENCE: LSD-07416

; CURRENT APPLICATION NUMBER: US/10/267,502

; CURRENT FILING DATE: 2003-01-27

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 429

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-267-502-429

Query Match 98.1%; Score 5810; DB 12; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 1e-283;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:           |:   : ||||||||||||||||||||||||||||
Db    181 SSGSVDETTLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNNQQELPTALTCLKVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKEPFRVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKEPFRVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

Qy    467 PLLEDPTSSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 526
      ||| ||||| ||||||||||||||||||||||||||||
Db    481 PLLGDPTSSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 540

Qy    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

Qy    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660

Qy    647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE 705
      ||||| ||||||||||||||||||||||||||||
Db    661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE 720

Qy    706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETS FESMI 765
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETS FESMI 780
```



Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS SKVLLLPDVSALGH 945  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS SKVLLLPDVSALA- 959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSTDEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLES 1065  
 Db 1020 VFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVILMWVFTYVGALFNGLT 1125  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVILMWVFTYVGALFNGLT 1139

Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 7

US-10-327-213-9

; Sequence 9, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-327-213-9

Query Match 98.1%; Score 5810; DB 16; Length 1192;

Best Local Similarity 97.2%; Pred. No. 1e-283;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 Db 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLS	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERWVEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERWVEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAIQVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAIQVTEKNTSTKTSNPPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFISKEAQIRETETFSOSSPIEIIIDEFPTLISSKTDSFSLKAREYTDLEVSHKSEI	885
Db	841	SNDDLFISKEAQIRETETFSOSSPIEIIIDEFPTLISSKTDSFSLKAREYTDLEVSHKSEI	900

QY 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH 945  
 |||  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA- 959  
 QY 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005  
 |||:|  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSALSKTSVVDLLYWRDIKKTGV 1019  
 QY 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065  
 |||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079  
 QY 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125  
 |||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139  
 QY 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 8

US-10-466-258-9

; Sequence 9, Application US/10466258  
 ; Publication No. US20040132096A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GLAXO GROUP LIMITED  
 ; TITLE OF INVENTION: ASSAY  
 ; FILE REFERENCE: P80966 GCW  
 ; CURRENT APPLICATION NUMBER: US/10/466,258  
 ; CURRENT FILING DATE: 2003-07-15  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-466-258-9

Query Match 98.1%; Score 5810; DB 16; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 1e-283;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

QY 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 |||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 QY 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120  
 |||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120  
 QY 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180  
 |||  
 Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180  
 QY 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226  
 |||:|:|

Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSP 240

Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286  
 |||||

Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy 287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV 346  
 |||||

Db 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

Qy 347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVVEVKDSKEDSDMLAAGGKIESNLESKV 406  
 |||||

Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVVEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy 407 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466  
 |||||

Db 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480

Qy 467 PLLEDPTSENXTDEKKIEEKKQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE 526  
 ||| |||||

Db 481 PLLGDPTSENKTDEKKIEEKKQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE 540

Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGTIAIYETKMDLVQTSEVMQESLYPAAQLCPSF 586  
 |||||

Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTIAIYETKMDLVQTSEVMQESLYPAAQLCPSF 600

Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 646  
 |||||

Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660

Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE 705  
 |||||

Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE 720

Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI 765  
 |||||

Db 721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI 780

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 |||||

Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 826 SNDDLFIKSEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 |||||

Db 841 SNDDLFIKSEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900

Qy 886 ANAPDGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGH 945  
 |||||

Db 901 ANAPDGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALA- 959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV 1005  
 ||||| :|

Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES 1065  
 |||||

Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFNGLT 1125  
 |||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFNGLT 1139  
 |||  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192  
 |||

RESULT 9

US-10-408-967-7

; Sequence 7, Application US/10408967  
 ; Publication No. US20040063161A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pharmacia & Upjohn Company  
 ; APPLICANT: Yan, Riqiang  
 ; APPLICANT: Lu, Yifeng  
 ; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease  
 ; FILE REFERENCE: 00925  
 ; CURRENT APPLICATION NUMBER: US/10/408,967  
 ; CURRENT FILING DATE: 2003-04-08  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-408-967-7

Query Match 97.8%; Score 5794; DB 12; Length 1192;  
 Best Local Similarity 97.0%; Pred. No. 6.6e-283;  
 Matches 1157; Conservative 4; Mismatches 16; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 |||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 |||  
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120  
 |||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120  
 |||  
 Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180  
 |||  
 Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180  
 |||  
 Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226  
 |||: | : |  
 Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240  
 |||  
 Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286  
 |||  
 Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300  
 |||  
 Qy 287 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV 346  
 |||  
 Db 301 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNNQQELPTALTCLKVKEDEVV 360  
 |||

Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLINTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFPAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 10  
 US-09-893-348-18  
 ; Sequence 18, Application US/09893348  
 ; Patent No. US20020072493A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal  
 ; APPLICANT: COHEN, Irun R.  
 ; APPLICANT: BESERMAN, Pierre  
 ; APPLICANT: MOSONEGO, Alon  
 ; APPLICANT: MOALEM, Gila  
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES  
 ; FILE REFERENCE: EIS-SCHWARTZ=2A  
 ; CURRENT APPLICATION NUMBER: US/09/893,348  
 ; CURRENT FILING DATE: 2001-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/314,161  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: US 09/218,277  
 ; PRIOR FILING DATE: 1998-12-22  
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715  
 ; PRIOR FILING DATE: 1998-07-21  
 ; PRIOR APPLICATION NUMBER: IL 124500  
 ; PRIOR FILING DATE: 1998-05-19  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 1163  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-893-348-18

Query Match 72.5%; Score 4296.5; DB 9; Length 1163;  
 Best Local Similarity 74.0%; Pred. No. 1.3e-207;  
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK	58
Db	1	MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEEDDEEEDDEDEDLEELEVLERK	60
Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSVSTVP	118
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL	224
Db	167	RGSGSVDETFLFALPAASEVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Qy	225	SPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS	284
Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDE	344

Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDSELEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Qy	464	NIFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTK	523
Db	456	NTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIQDVPQTEEAQVMLMKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTDSESKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESETFSDDSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSA	942
Db	871	SEIANIQSGADSLPCLLPCDLSEFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1107
Qy	1123	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178



Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163

RESULT 11

US-10-267-502-431

; Sequence 431, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 431  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-267-502-431

Query Match 72.2%; Score 4277.5; DB 12; Length 1163;  
Best Local Similarity 73.8%; Pred. No. 1.1e-206;  
Matches 883; Conservative 108; Mismatches 154; Indels 51; Gaps 19;

QY 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKP 59  
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Db 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEDEDEDLEELEVLERKP 60  
QY 60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA 119  
||||| ||| ||| |||:|| :| ||||| ||||| |||||: || :| |  
Db 61 AAGLSAVPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A 114  
QY 120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRR 179  
|| |||| ||||| ||||| || || || || ||||| |||||  
Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163  
QY 180 GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP SLS 225  
|| : ||||| |||||:|:||||| ||||| |||||  
Db 164 GSGSVDETLFALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLP SLS 223  
QY 226 PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE 285  
||| |||| ||||| | ||||:| :|||:| :| :||| |||||  
Db 224 PLSTVSFKEHGYLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE 283  
QY 286 MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEV 345  
|||||: ||| |||:| | :|||:|:|:|:| | : || || | |||:|||| |  
Db 284 MGSSFNKSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTCLKVKEDEV 342  
QY 346 VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404  
:| || | ||| :|| ||:||||| |||||: ||||| :| ||| :|||  
Db 343 MSPEKTMDFNEMKMSVVAPVREEYADFKPFEQAWVEVKDITYEGSRDVLAA----RANMES 398  
QY 405 KVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN 464  
|||||| ||||| :| ||||| ||: ||||| :|| | ||||| | :||| | |  
Db 399 KVDKKCFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFT-SATESTAAN 457

Qy 465 IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLT KV 524  
 Db 458 IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVVAIHDSEADYVTTDNLSKV 516

Qy 525 TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584  
 Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP 576

Qy 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPP 643  
 Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPENPP 636

Qy 644 PYEEAMSVSLKVSIGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDY 703  
 Db 637 PYEEAMSVALKTSDAKEEIKEPESFNAAAQAEAPYISIACDLIKETKLSTEPSGFSNY 696

Qy 704 SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFS 763  
 Db 697 SEIAKFEKSVPDPHCELVDSSPESEPVDFLFSDDSIQEVPTQEEAVMLMKESLTEVS-ET 755

Qy 764 MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823  
 Db 756 VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA 814

Qy 824 VYSNDDLFISKEAQIRETETFSDDSSPIEIDEFPTLISSKTDSFSKLAREYTDLEVSHKS 883  
 Db 815 IYSNDDLSSKEDKMKESETFSDSSPIEIDEFPTFVSAKDDS----PKEYTDLEVS NKS 870

Qy 884 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS KVL LPPDV SAL 943  
 Db 871 EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPLLLPNVSAL 928

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSTDEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKT 1003  
 Db 929 -ESQIEMGNIVKPKVLTKEAEKKLPSTDEKEDRSLTAVLSAELNKT SVVDLLYWRDIKKT 987

Qy 1004 GVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1062  
 Db 988 GVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFVLMWVFTYVGALFN 1122  
 Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLVDLKFVLMWVFTYVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 Db 1108 GLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1163

RESULT 12

US-09-789-386-6

; Sequence 6, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

```

; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6

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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN 240
        |||:|
Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
        ||
Db    186 ----- 185

QY    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
        ||
Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
        ||
Db    186 ----- 185

QY    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTDE 480
        ||
Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL 540
        ||
Db    186 ----- 185

```

QY 541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600  
 Db 186 ----- 185  
 QY 601 VMEAPLNSAVPSAGASVIQPS SSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660  
 Db 186 ----- 185  
 QY 661 EIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV 720  
 Db 186 ----- 185  
 QY 721 EDSSPDSEPVDLFSDD SIPDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG 780  
 Db 186 ----- 185  
 QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDL FISK EAQIRE 840  
 Db 186 ----- 185  
 QY 841 TETFSDSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900  
 Db 186 ----- 185  
 QY 901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLE 960  
 Db 186 ----- 185  
 QY 961 KEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASL FLLLSLTVF 1020  
 Db 186 -----VVDLLYWRDIKKTGVVFGASL FLLLSLTVF 215  
 QY 1021 SIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080  
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275  
 QY 1081 ALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140  
 Db 276 ALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335  
 QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 13

US-09-765-205-6

; Sequence 6, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: human  
US-09-765-205-6

Query Match 25.2%; Score 1495.5; DB 9; Length 373;  
Best Local Similarity 31.6%; Pred. No. 2e-67;  
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLGN 240
          |||:|
Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
          ||
Db    186 ----- 185

QY    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
          ||
Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
          ||
Db    186 ----- 185

QY    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDE 480
          ||
Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL 540
          ||
Db    186 ----- 185

QY    541 VQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFESEATPSPVLPDI 600
          ||
Db    186 ----- 185

QY    601 VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
          ||
Db    186 ----- 185
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QY 661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVDPDHSELV 720  
 Db 186 ----- 185  
 QY 721 EDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780  
 Db 186 ----- 185  
 QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE 840  
 Db 186 ----- 185  
 QY 841 TETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900  
 Db 186 ----- 185  
 QY 901 PHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLLPPDVVSALGHTQAEIESIVKPKVLE 960  
 Db 186 ----- 185  
 QY 961 KEAEKKLPDTEKEDRSPSAIFSDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020  
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215  
 QY 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080  
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275  
 QY 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140  
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335  
 QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 14

US-09-893-348-24

; Sequence 24, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

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; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

QY    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPNTISAGQEDFPSVLLETAASXPSLSPLSAA SFKEHEYLGN 240
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Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGS SFSVSPKAESAV 300
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Db    186 ----- 185

QY    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALT KLVKEDEVVSSEKAKDSFNEKRV 360
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Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV DKKCFADSLEQTNH 420
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Db    186 ----- 185

QY    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF P LLEDPTS ENXTDE 480
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Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVT TDNLTKVTEEVVANMPEGLTPDL 540
        -----
Db    186 ----- 185

QY    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS FE ESEATPSPVLPDI 600
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Db    186 ----- 185

QY    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPP YEEAMSVSLKVSGIKE 660

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Db 186 ----- 185  
 QY 661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV 720  
 Db 186 ----- 185  
 QY 721 EDSSPDSEPVDFLSDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780  
 Db 186 ----- 185  
 QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840  
 Db 186 ----- 185  
 QY 841 TETFSOSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900  
 Db 186 ----- 185  
 QY 901 PHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLE 960  
 Db 186 ----- 185  
 QY 961 KEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020  
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215  
 QY 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNS 1080  
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNS 275  
 QY 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140  
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335  
 QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 15

US-10-408-967-8

; Sequence 8, Application US/10408967

; Publication No. US20040063161A1

; GENERAL INFORMATION:

; APPLICANT: Pharmacia & Upjohn Company

; APPLICANT: Yan, Riqiang

; APPLICANT: Lu, Yifeng

; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease

; FILE REFERENCE: 00925

; CURRENT APPLICATION NUMBER: US/10/408,967

; CURRENT FILING DATE: 2003-04-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens



US-10-408-967-8

Query Match 25.2%; Score 1495.5; DB 12; Length 373;  
Best Local Similarity 31.6%; Pred. No. 2e-67;  
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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QY      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

QY     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

QY    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

QY    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN 240
          |||:|
Db    181 SSGSV----- 185

QY    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
          ||
Db    186 ----- 185

QY    301 IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
          ||
Db    186 ----- 185

QY    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
          ||
Db    186 ----- 185

QY    421 EKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDE 480
          ||
Db    186 ----- 185

QY    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
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Db    186 ----- 185

QY    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
          ||
Db    186 ----- 185

QY    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
          ||
Db    186 ----- 185

QY    661 EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV 720
          ||
Db    186 ----- 185

QY    721 EDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
          ||
Db    186 ----- 185
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Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI	840
Db	186	-----	185
Qy	841	TETFSOSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	186	-----	185
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	186	-----	185
Qy	961	KEAEKKLPDTEKEDRSPSAIFSDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	186	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF	215
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	216	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	275
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	276	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	335
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	336	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	373

Search completed: September 3, 2004, 16:30:08  
 Job time : 123.281 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:59:39 ; Search time 74.0403 Seconds  
(without alignments)  
5019.975 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaphage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description
<hr/>						

1	4851	81.9	986	4	Q8IUA4	Q8iua4 homo sapien
2	4289	72.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
3	4277.5	72.2	1163	11	Q8K3G8	Q8k3g8 mus musculu
4	3658.5	61.8	1046	11	Q8BGK7	Q8bgk7 mus musculu
5	2580.5	43.6	720	11	Q7TNB7	Q7tnb7 mus musculu
6	2527	42.7	639	11	Q8K290	Q8k290 mus musculu
7	2233	37.7	578	11	Q80W95	Q80w95 mus musculu
8	1531	25.8	392	4	Q96B16	Q96b16 homo sapien
9	1201.5	20.3	375	11	Q8BHF5	Q8bhf5 mus musculu
10	1163	19.6	356	11	Q8BH78	Q8bh78 mus musculu
11	1152.5	19.5	357	11	Q8K3G7	Q8k3g7 mus musculu
12	901	15.2	184	6	Q7YRW9	Q7yrw9 bos taurus
13	887	15.0	199	13	Q7T224	Q7t224 gallus gall
14	867	14.6	179	6	Q9GM33	Q9gm33 macaca fasc
15	788.5	13.3	760	13	Q90638	Q90638 gallus gall
16	779	13.2	780	11	Q8K4S4	Q8k4s4 mus musculu
17	778	13.1	780	11	Q8K0T0	Q8k0t0 mus musculu
18	755.5	12.8	214	13	Q7T222	Q7t222 carassius a
19	699	11.8	643	11	Q8CCU2	Q8ccu2 mus musculu
20	688	11.6	199	4	Q9BQ59	Q9bq59 homo sapien
21	672	11.3	208	13	Q90637	Q90637 gallus gall
22	671	11.3	267	11	Q63765	Q63765 rattus sp.
23	626	10.6	237	11	Q8C6D5	Q8c6d5 mus musculu
24	623.5	10.5	236	11	Q8VBU0	Q8vbu0 rattus norv
25	586	9.9	221	13	Q7ZUD6	Q7zud6 brachydanio
26	566	9.6	595	5	Q9VMV9	Q9vmv9 drosophila
27	528	8.9	234	5	Q9VMW3	Q9vmw3 drosophila
28	528	8.9	2484	5	Q9U347	Q9u347 caenorhabdi
29	526	8.9	224	5	Q9VMW1	Q9vmw1 drosophila
30	520	8.8	222	5	Q9VMW4	Q9vmw4 drosophila
31	519.5	8.8	2607	5	Q23187	Q23187 caenorhabdi
32	518	8.7	202	5	Q9VMW2	Q9vmw2 drosophila
33	358.5	6.1	1417	3	Q871Y7	Q871y7 neurospora
34	357.5	6.0	2768	5	Q9VC00	Q9vc00 drosophila
35	343	5.8	107	13	Q7T223	Q7t223 carassius a
36	341.5	5.8	5412	5	Q9W596	Q9w596 drosophila
37	340.5	5.7	222	5	Q23188	Q23188 caenorhabdi
38	339	5.7	1150	5	Q8IMM6	Q8imm6 drosophila
39	334	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila
40	334	5.6	18074	5	Q9I7U4	Q9i7u4 drosophila
41	331	5.6	7962	4	Q10465	Q10465 homo sapien
42	331	5.6	34350	4	Q8WZ42	Q8wz42 homo sapien
43	325.5	5.5	5327	5	O76891	O76891 drosophila
44	322.5	5.4	846	5	Q8MRP6	Q8mrp6 drosophila
45	322.5	5.4	1109	5	Q9VAY4	Q9vay4 drosophila

# ALIGNMENTS

## RESULT 1

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.

AC Q8IUA4;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)



Qy	373	FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTS	432
Db	181	FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTS	240
Qy	433	FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDEKKIEEKKQIVT	492
Db	241	FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDPTSENKTDEKKIEEKKQIVT	300
Qy	493	EKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEV	552
Db	301	EKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEV	360
Qy	553	TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDIVMEAPLNSAVPS	612
Db	361	TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDIVMEAPLNSAVPS	420
Qy	613	AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL-KVSGIKEEIKEPENINAA	671
Db	421	AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAA	480
Qy	672	LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVD	731
Db	481	LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVD	540
Qy	732	LFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS	791
Db	541	LFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS	600
Qy	792	LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIE	851
Db	601	LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIE	660
Qy	852	IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP	911
Db	661	IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP	720
Qy	912	KVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPST	971
Db	721	KVEEKISFSDDFSKNGSATSQVLLLPDVSALA-TQAEIESIVKPKVLVKEAEKKLPST	779
Qy	972	EKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL	1031
		:	
Db	780	EKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL	839
Qy	1032	ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE	1091
Db	840	ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE	899
Qy	1092	LRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY	1151
Db	900	LRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY	959
Qy	1152	LGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	960	LGLANKNVKDAMAKIQAKIPGLKRKAE	986

# RESULT 2

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
AC Q8BGM9;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
RT Structures of Human and Mouse Nogo/Rtn-4.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY102284; AAM73506.1; -.  
DR EMBL; AY102286; AAM73511.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1162 AA; 126613 MW; 855697FBEE11781F CRC64;

Query Match 72.4%; Score 4289; DB 11; Length 1162;  
Best Local Similarity 73.9%; Pred. No. 1.7e-203;  
Matches 883; Conservative 109; Mismatches 153; Indels 50; Gaps 18;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP 59  
| | | : | | | | | | | | | | | | | | | : | | : | | | | | | | | | | | |  
Db 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDLEELEVLERKP 60  
Qy 60 AAGLSAAPVPTAPAAPAGPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA 119  
| | | | | | | | | | | | | | | : | | | | | | | | | | | | | | : | | | |  
Db 61 AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A 114

Qy 120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRR 179  
 || ||| ||||| ||||| || || || || ||||| ||||| |||||

Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163

Qy 180 GSSG-----AVVXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP SLS 225  
 || : ||||| ||||| : ||||| ||||| ||||| |||||

Db 164 GSGSVDET LFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLS 223

Qy 226 PLSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE 285  
 ||| ||||| ||||| | ||||:| :|||:| :| :||| :||| ||| |||||

Db 224 PLSTVSFKEHGYLGNLSAVASTEGTIEETLINEASRELPERATNPFVNRESAEFSVLEYSE 283

Qy 286 MGSSFVSVPKAE SAVIVANPREEIVKKNKDEEEKLVSNILHXQQELPTALT KLKVEDEV 345  
 |||||: ||| |||:| | :||:|:|:|:| : || : || | |||:|||| |

Db 284 MGSSFNGSPKGESAM LVENTKKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVKEDGV 342

Qy 346 VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404  
 :| || | ||| :||:| ||:|||||||: ||||: | | |:||| :||:|

Db 343 MSPEKTMDIFNEMKMSV VAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANMES 398

Qy 405 KVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN 464  
 ||||| ||||| | ||||| |:: ||| ||| :|| | ||||| | : :||| | |

Db 399 KVDKKCFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFS-SATESTAAN 457

Qy 465 IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT KV 524  
 |||:|| | ||| |||||:||||:|| | | ||||| || ||| |||||:||

Db 458 IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIH DSEADYVTTDNLSKV 516

Qy 525 TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584  
 || ||| ||||| ||||| ||||| ||||| |||||:||||| :|||:|| |||||

Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP 576

Qy 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS SSPLEA-SSVNYESIKHEPENPP 643  
 ||||:||||| ||||| :|| |||| |||:|||| | |:|: || |||||

Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPP 636

Qy 644 PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYIS IACDLIKETKLSAEPAPDFSDY 703  
 |||||:|| | |||||: ||| ||| ||||| ||||| |||||:|||:|

Db 637 PYEEAMSVALKTSDSKEEIKEPESFNAAAQEA EAPYIS IACDLIKETKLSTEPSPEFSNY 696

Qy 704 SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FES 763  
 ||:|| |: |||| |||:||||:||||| ||||:|| |:| |||:|||| | |:

Db 697 SEIAKFEKSVDPDHCELVDDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL TEVS-ET 755

Qy 764 MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823  
 : :||:||| | | |||||: :| ||| :||: ||| | ||||| :||

Db 756 VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLT KKETISLQMEEFNTA 814

Qy 824 VYSNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKS 883  
 :||||| ||| :||:||||| ||||| :|| || :|||||:||

Db 815 IYSNDDLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDS----PKEYTDLEVS NKS 870

Qy 884 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPDVSAL 943  
 |||| | ||||:||| ||| || | : ||:|||| |: ||| || |:||||

Db 871 EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEF SKSRSSSVSKVPLLLPNVSAL 928

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKT 1003





Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS	225
Db	164	GSGSVDETLFALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLS	223
Qy	226	PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE	285
Db	224	PLSTVSFKEHGYLGNLSAVASTEGETIETLNEASRELPERATNPFVNRESAEFSVLEYSE	283
Qy	286	MGSSFSVSPKAESAVIVANPREELIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEV	345
Db	284	MGSSFNKSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV	342
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES	404
Db	343	MSPEKTMDIFNEMKMSVVPVREEYADFKPFEQAWEVKDTYEGSRDLVLA-----RANMES	398
Qy	405	KVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN	464
Db	399	KVDKKCFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFT-SATESTAAN	457
Qy	465	IFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKV	524
Db	458	IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPPFLVAIHDEADYVTTDNLISKV	516
Qy	525	TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCP	584
Db	517	TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSSEAIQESIYPTAQLCP	576
Qy	585	SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPP	643
Db	577	SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPP	636
Qy	644	PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDY	703
Db	637	PYEEAMSVALKTSDAKEEIKEPESFNAAAQAEAPYISIIACDLIKETKLSTEPSPGFSNY	696
Qy	704	SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFES	763
Db	697	SEIAKFEKSVDPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ET	755
Qy	764	MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA	823
Db	756	VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA	814
Qy	824	VYSNDDLFIKSEAQIRETETFSDDSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKS	883
Db	815	IYSNDDLSSKEDKMKESETFSDSPIEIIIDEFPTFVSAKDDS----PKEYTDLEVSNKS	870
Qy	884	EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA	943
Db	871	EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFSKSRSSSVSKVPLLLPNVSAL	928
Qy	944	GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKT	1003



DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 61.8%; Score 3658.5; DB 11; Length 1046;

Best Local Similarity 69.5%; Pred. No. 2e-172;

Matches 767; Conservative 108; Mismatches 148; Indels 81; Gaps 17;

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Qy      97 APPVAPERQ-----PSWDPS-----PVSSTVPAP---SPLSAAAVSPSKLPED 136
      |||:| | :| || | | | | | | | | |
Db      2 APPLAGGGQKGGAASEAWVPSLFGVSGSTCTAAKSLVPIPARSSRLSAA----- 51

Qy     137 DEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLK 196
      : | :: || | : | | :: : | | | |
Db      52 -----RNETLFALPA---ASEPVISSAE-----KIMDLK 78

Qy     197 EQPGNTISAGQEDFPSVLLETAASXPSSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENV 256
      ||| |||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      79 EQPGNTVSSGQEDFPSVLFFETAASLPSLSPLSTVSFKEHGYLGNLSAVASTEGTIEETLN 138

Qy     257 EASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVKNKDE 316
      |||:|: | :| :|: | | | | | | | | | | | | | | | | | | | | | |
Db     139 EASRELPERATNPFVNRESAEFSVLEYSEMGSFSNGSPKGESAMLVENTKEEVIVRSKDK 198

Qy     317 EEKLVSNILHXQQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376
      | : || : || | | | | | | | | | | | | | | | | | | | | | | | |
Db     199 ED-LVCSAALHNPQESPATLTQVVKEDGVMSPEKTMDIFNEMKMSVVAPVREEYADFKPF 257

Qy     377 ERVWEVKDSKEDS-DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPS 435
      | : | | | | : | | | : | | | | | | | | | | | | | | | | | | | |
Db     258 EQAWEVKDTYEGSRDVLAA----RANMESKVDKKCFEDSLEQKGHGKDSSESRNENASFPR 313

Qy     436 TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKN 495
      ||| :| | | | | | | :| | | | | | | | | | | | | | | | | | | |
Db     314 TPELVKDGSRAYITCDSFS-SATESTAANIFFVLEDHTSENKTDEKKIEERKAQIITEK- 371

Qy     496 TSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEVTGT 555
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     372 TSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACESELNEATGT 431

Qy     556 KIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGA 615
      ||| |||:| | | | | :| | :| | | | | | | | | | | | | | | | | |
Db     432 KIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGA 491

Qy     616 SVIQPSSSPLEA-SSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAALQE 674
      || | | | :| | | | | | :| :| | | | | | | | | | | | | | | | |
Db     492 SVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQE 551

Qy     675 TEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS 734
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     552 AEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVDPDHCELVDSSPESEPVDLFS 611

Qy     735 DDSIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDN 794
      ||| |||:| | | | | | | | | | | | :| :| :| :| :| | | | | | |
Db     612 DDSIPEVPQTQEEAVMLMKESLTEVS-ETVTQHKHKERLSASQVEVGKPYLESFQPNLHI 670

Qy     795 TKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDDSPIEIID 854
      ||| :| :| | | | | | | | | | | | | | | | | | | | | | | | | |
```

Db 671 TKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDLSSKEDKMKESETFSDSSPIEIID 729

Qy 855 EFPTLISSKTDSEFSKLAAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE 914  
 |||| :|:| || :|||||||:||||| || ||||:|| || || || ||

Db 730 EFPTFVSAKDDSD---PKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE 785

Qy 915 EKISFSDDFSKNKSATSQVLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPDTEKE 974  
 : ||:||||: |: || || || |:|||| :| |: :||||| ||||:|||||||

Db 786 AHV--SDEFSKSRSSSVSKVPLLLPNVSAL-ESQIEMGNIVKPKVLTKEAEKLPDTEKE 842

Qy 975 DRSPSAIFSA DLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034  
 ||| :|: ||:| |||||||||||||||||||||||||||||||||||||||

Db 843 DRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 902

Qy 1035 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094  
 ||||||||||||||||||||||||||||||||||||||| |||||

Db 903 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 962

Qy 1095 LFLVDDLVDL SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154  
 |||||||||||||||||||||||||||||||||||:|||||||||

Db 963 LFLVDDLVDL SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 1022

Qy 1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||:|||||||||||||||||

Db 1023 ANKSVKDAMAKIQAKIPGLKRKAE 1046

RESULT 5

Q7TNB7

ID Q7TNB7 PRELIMINARY; PRT; 720 AA.

AC Q7TNB7;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC056373; AAH56373.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;

Query Match 43.6%; Score 2580.5; DB 11; Length 720;  
 Best Local Similarity 70.8%; Pred. No. 2.1e-119;  
 Matches 527; Conservative 69; Mismatches 107; Indels 41; Gaps 13;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		:                            : : : : : : : : : : : :	
Db	1	MEDIDQSSSLVSSSADSPPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		:                     :    :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP SLS	225
		:            : : : : : :	
Db	164	GSGSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFE TAASLPSLS	223
Qy	226	PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE	285
		:  : : : : : :  : :	
Db	224	PLSTVSFKEHGYLGNLSAVASTEGTIEETLINEASRELPERATNPFVNRESAEFSVLEYSE	283
Qy	286	MGSSFSVSPKAESAVIVANPREEIIVKNKDDEEEKLVSNNILHXQQELPTALTCLKVKEDEV	345
		:        :    : : : : : : :    :            :	
Db	284	MGSSFNGSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV	342
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES	404
		:           : :    : : : : : : : : :       :    : :	
Db	343	MSPEKTMDIFNEMKMSV VAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANMES	398
Qy	405	KVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN	464
		: :         :           : :	
Db	399	KVDKKCFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFS-SATESTAAN	457
Qy	465	IFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT KV	524
		:             : : : :                      :	
Db	458	IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIH DSEADYVTTDNLSKV	516
Qy	525	TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP	584
		: : : :	



Qy	711	QPVPDHSELVEDSSPDSEPVDLFSDSDSI	PDVPQKQDETVMVLVKESLTETSFESMIEYENK	770
Db	181	KSVDPDHCELVDSSPESEPVDLFSDSDSI	PEVPQTQEEAVMLMKESLTEVS-ETVTQHKHK	239
Qy	771	EKLSALPPEGGKPYLESFKLSLDNTKDTLLP	DEVSTLSKKEKIPLOMEELSTAVYSNDDL	830
Db	240	ERLSASPQEVGKPYLESFQPNLHITKDA-ASNEI	PTLTKKETISLQMEEFNTAIYSNDDL	298
Qy	831	FISKEAQIRETETTFSDSSPIEIIIDFPTL	ISSKTDSEFSKLAREYTDLEVSHKSEIANAPD	890
Db	299	LSSKEDKMKESETFSDSSPIEIIIDFPTFVS	AKDDS---PKEYTDLEVSNKSEIANVQS	354
Qy	891	GAGSLPCTELPHDLSLKNIQPKVEEKISFSD	DFSKNGSATSKVLLLPPDV	950
Db	355	GANSLPCSELPCDLSFKNTYPKDEAHV--SDE	FSKSRSSSVKVPLLLPNVSAL-ESQIEM	411
Qy	951	ESIVKPKVLEKEAEKKLPDTEKEDRSPSAI	FADLGKTSVVDLLYWRDIKKTGVVFGAS	1010
Db	412	GNIVKPKVLTKEAEKKLPDTEKEDRSLTAVL	SAELNKTSVVDLLYWRDIKKTGVVFGAS	471
Qy	1011	LFLLLSLTVFSIVSVTAYIALALLSVTISFRI	YKGVIAIQKSDEGHPFRAYLESEVAIS	1070
Db	472	LFLLLSLTVFSIVSVTAYIALALLSVTISFRI	YKGVIAIQKSDEGHPFRAYLESEVAIS	531
Qy	1071	EELVQKYSNSALGHVNCTIKELRRLFLVDDL	LVDSLKFAVLMWVFTYVGALFNGLTLLILA	1130
Db	532	EELVQKYSNSALGHVNSTIKELRRLFLVDDL	LVDSLKFAVLMWVFTYVGALFNGLTLLILA	591
Qy	1131	LISLFSVPVIYERHQAQIDHYLGLANKNVKDA	MAKIQAKIPGLKRKAE	1178
Db	592	LISLFSIPVIYERHQAQIDHYLGLANKSVKDA	MAKIOAKIPGLKRKAE	639

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Q80W95
ID   Q80W95          PRELIMINARY;          PRT;    578 AA.
AC   Q80W95;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-A (Fragment).
GN   NOGO-A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tozaki H., Hirata T.;
RT   "The partial sequence of mouse nogo-A cDNA clone#4109.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB073672; BAC75974.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.

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ID      Q80W95                PRELIMINARY;          PRT;    578 AA.
AC      Q80W95;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nogo-A (Fragment).
GN      NOGO-A.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tozaki H., Hirata T.;
RT      "The partial sequence of mouse nogo-A cDNA clone#4109.";
RL      Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AB073672; BAC75974.1; -.
DR      GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.

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FT NON\_TER 1 1  
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 37.7%; Score 2233; DB 11; Length 578;  
Best Local Similarity 78.4%; Pred. No. 2.2e-102;  
Matches 460; Conservative 52; Mismatches 65; Indels 10; Gaps 6;

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Qy      593 PSPVLPDIVMEAPLNSAVPSAGASVIQPSSSSPLEA-SSVNYESIKHEPENPPPPYEEAMSV 651
          ||||| :|| ||| ||:|||| | |:| || |||||
Db      1 PSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPPYEEAMSV 60

Qy      652 SLKVSIGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQ 711
          :|| | |||||: ||| || ||||| ||||| ||:| ||:||||:| | :
Db      61 ALKTSDAKEEIKEPESFNAAAQAEAPYISIIACDLIKETKLSTEPSPGFSNYSEIAKFEK 120

Qy      712 PVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKE 771
          ||| |||:||||:|||||:|||| |:| |||:|||| | |:| :::||
Db      121 SVPDHCELVDSSPESEFPVDLFSDDSIPEVPQTQEEAVMLMKESLTVS-ETVTQHKHKE 179

Qy      772 KLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLF 831
          :||| | |||||: :| ||| :| ||:|||| | |||| :||:|||||
Db      180 RLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDLL 238

Qy      832 ISKEAQIRETETFSDDSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDG 891
          ||| ::|:|||||:||||| :|:| || :|||||:||||| |
Db      239 SSKEDKMKESETFSDDSPIEIIIDEFPTFVSAKDDS---PKEYTDLEVSNNKSEIANVQSG 294

Qy      892 AGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLLPPDVSA LGHTQAEIE 951
          | ||||:|||| ||| || | | : ||:|||| |: | || || |:|||| :| |:
Db      295 ANSLPCSELPCDLSFKNTYPKDEAHV--SDEFSSKSRSSVFKVPLLLPNVSAL-ESQIEMG 351

Qy      952 SIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL 1011
          :||||| ||||:|||||:|||| :|: ||:| ||||| |||||
Db      352 NIVKPKVLTKEAEKKLPSDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASL 411

Qy      1012 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      412 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 471

Qy      1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 1131
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      472 ELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 531

Qy      1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      532 ISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 578
```

RESULT 8

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.  
AC Q96B16;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein (RTN4).  
GN RTN4.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22376540; PubMed=12488097;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL J. Mol. Biol. 325:299-323(2003).  
 DR EMBL; BC016165; AAH16165.1; -.  
 DR EMBL; AY102285; AAM64242.1; -.  
 DR EMBL; AY102278; AAM64247.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 25.8%; Score 1531; DB 4; Length 392;  
 Best Local Similarity 32.4%; Pred. No. 6.1e-68;  
 Matches 382; Conservative 7; Mismatches 3; Indels 786; Gaps 4;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP 120  
 Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKRRG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKRRG 180  
 Qy 181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLETAASXPSLSPLSAASFKEHEYLGN 240

Db	181	SSGSV-----	185
Qy	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV	300
Db	186	-----	185
Qy	301	IVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV	360
Db	186	-----	185
Qy	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH	420
Db	186	-----	185
Qy	421	EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTDE	480
Db	186	-----DETLE-----	190
Qy	481	KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL	540
Db	191	-----	190
Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	191	-----	190
Qy	601	VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	191	-----ALPAA-----	195
Qy	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	196	-----	195
Qy	721	EDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Db	196	-----SEPV-----	199
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE	840
Db	200	-----	199
Qy	841	TETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	200	-----	199
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	200	-----	199
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	200	-----IRSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	234
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080

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Db          235 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 294
QY          1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
            |||
Db          295 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 354
QY          1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
            |||
Db          355 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392

```

RESULT 9

Q8BHF5

```

ID   Q8BHF5          PRELIMINARY;          PRT;    375 AA.
AC   Q8BHF5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102282; AAM73504.1; -.
DR   EMBL; AY102286; AAM73509.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE    375 AA;  40300 MW;  23D9EB19BE671AE6 CRC64;

```

Query Match 20.3%; Score 1201.5; DB 11; Length 375;

Best Local Similarity 28.6%; Pred. No. 1.1e-51;  
Matches 337; Conservative 17; Mismatches 20; Indels 805; Gaps 11;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
Db	1	MEDIDQSSLVSSSADSPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDELEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPA	119
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLKVEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD	479
Db	166	-----GSVDETLF-----	173
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD	539
Db	174	-----	173
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPD	599
Db	174	-----	173
Qy	600	IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK	659
Db	174	-----ALPAA-----	178
Qy	660	EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL	719
Db	179	-----	178
Qy	720	VEDSSPDSEPVDLFSDDSIQDPVQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE	779
Db	179	-----SEPV-----	182
Qy	780	GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKESKAQIR	839

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Db      183 ----- 182
Qy      840 ETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899
Db      183 ----- 182
Qy      900 LPHDLSLKNIQPKVEEKISFSDDFSKNKSATSKVLLLPPDVSALGHTQAEIESIVKPKVL 959
Db      183 ----- 182
Qy      960 EKEAEKKLPSDTEKEDRSPSAIFSAIDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTV 1019
          :||                               ::|||
Db      183 -----IPS-----SAVVDLLYWRDIKKTGVVFGASLFLLLSLTV 216
Qy      1020 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 1079
          |||
Db      217 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 276
Qy      1080 SALGHVNCTIKELRRLFLVDDLVDSLKFVAVLMWVFTYVGALENGLTLLILALISLFSVPV 1139
          |||
Db      277 SALGHVNSTIKELRRLFLVDDLVDSLKFVAVLMWVFTYVGALENGLTLLILALISLFSIPV 336
Qy      1140 IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||
Db      337 IYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 375

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RESULT 10

Q8BH78

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ID   Q8BH78          PRELIMINARY;      PRT;   356 AA.
AC   Q8BH78;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

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RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY102281; AAM73503.1; -.  
 DR EMBL; AY102286; AAM73508.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 19.6%; Score 1163; DB 11; Length 356;  
 Best Local Similarity 27.7%; Pred. No. 8e-50;  
 Matches 326; Conservative 12; Mismatches 17; Indels 824; Gaps 8;

Qy	1	MEDLDQSPVLSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		:                            :    :    :	
Db	1	MEDIDQSSVLSSSADSPRPPLPAFKYQFVTEPEDEEDEDEEEEEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		:                     :    :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS--A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPFAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPD	599

Db 166 ----- 165  
 Qy 600 IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVS GIK 659  
 Db 166 ----- 165  
 Qy 660 EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSEL 719  
 Db 166 ----- 165  
 Qy 720 VEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPE 779  
 Db 166 ----- 165  
 Qy 780 G GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDL FISK EAQIR 839  
 Db 166 ----- 165  
 Qy 840 ETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899  
 Db 166 ----- 168  
 Qy 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLLPPDV SALGHTQAEIESIVKPKVL 959  
 Db 169 ----- 168  
 Qy 960 EKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASL FLLLSLTV 1019  
 Db 169 ----- 197  
 Qy 1020 FSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSN 1079  
 Db 198 FSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSN 257  
 Qy 1080 SALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPV 1139  
 Db 258 SALGHVNSTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPV 317  
 Qy 1140 IYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178  
 Db 318 IYERHQAQIDHYLGLANKSVKDAMAKIQA KIPGLKRKAE 356

RESULT 11

Q8K3G7

ID Q8K3G7 PRELIMINARY; PRT; 357 AA.

AC Q8K3G7;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nogo-B.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]



RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Jin W., Li R., Long M., Shen J., Ju G.;  
 RT "Cloning and expression of the mouse Nogo-B protein."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY114153; AAM77069.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 19.5%; Score 1152.5; DB 11; Length 357;  
 Best Local Similarity 27.6%; Pred. No. 2.6e-49;  
 Matches 326; Conservative 12; Mismatches 17; Indels 825; Gaps 9;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		:                      : :    :	
Db	1	MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		:                     :    :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPSTPAAPKRR	179
Db	115	PSLPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSPFEESEATPSPVLPD	599
Db	166	-----	165

Qy 600 IVMEAPLNSAVPSAGASVIQPS SSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK 659

Db 166 ----- 165

Qy 660 EEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSEL 719

Db 166 ----- 165

Qy 720 VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE 779

Db 166 ----- 165

Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIR 839

Db 166 ----- 165

Qy 840 ETETFS DSSPIEIIDEFP TLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899

Db 166 ----- ||: GSV---- 168

Qy 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALGHTQAEIESIVKPKVL 959

Db 169 ----- 168

Qy 960 EKEAEKKLP SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVV-FGASL FLLLSLT 1018

Db 169 ----- ||||| ||||| VVDLLYWRDIKKTGVVYFGASL FLLLSLT 197

Qy 1019 VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYS 1078

Db 198 VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYS 257

Qy 1079 NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP 1138

Db 258 NSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 317

Qy 1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

Db 318 VIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 357

# RESULT 12

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.

AC Q7YRW9;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4w (Fragment).

GN RTN4.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

```

RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; AY164744; AAP47319.1; -.
FT      NON_TER      1      1
SQ      SEQUENCE      184 AA;  20671 MW;  DE990E03BBAF84A1 CRC64;

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Qy	995	LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSD	1054
Db	1	LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSD	60
Qy	1055	EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF	1114
Db	61	EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF	120
Qy	1115	TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLK	1174
Db	121	TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLK	180
Qy	1175	RKAE	1178
Db	181	RKAE	184

07T224

Query Match 15.0%; Score 887; DB 13; Length 199;  
Best Local Similarity 88.2%; Pred. No. 1.6e-36;

Matches 180; Conservative 7; Mismatches 11; Indels 6; Gaps 1;

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Qy      975 DRSPSAIFSadLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034
      |  ||      |  |||
Db      2 DSQPSG-----WKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 55

Qy     1035 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094
      |||
Db      56 SVTISFRIYKGVIAIQKSDEGHPFRAYLESdVAVSEDLIQKYSSVVLGHINGTVKELRR 115

Qy     1095 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154
      |||
Db     116 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 175

Qy     1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178
      |||
Db     176 VNKNVKDAMAKIQAKIPGLKRKTE 199
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RESULT 14

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.  
AC Q9GM33;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; *Macaca*.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB049853; BAB16739.1; -.  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 14.6%; Score 867; DB 6; Length 179;  
Best Local Similarity 98.3%; Pred. No. 1.3e-35;  
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy     1000 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPF 1059
      :|||
Db      1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRQVIAIQKSDEGHPF 60

Qy     1060 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 1119
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      |||
Db      61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLRFVLMWVFTYVGA 120
      |||
Qy      1120 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
      |||
Db      121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179
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RESULT 15

Q90638

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ID      Q90638      PRELIMINARY;      PRT;      760 AA.
AC      Q90638;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      ChS-Rex-b (RTN1-A).
GN      RTN1.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=96386034; PubMed=8793864;
RA      Baka I.D., Ninkina N.N., Pinon L.G., Adu J., Davies A.M.,
RA      Georgiev G.P., Buchman V.L.;
RT      "Intracellular compartmentalization of two differentially spliced s-
RT      rex/NSP mRNAs in neurons.";
RL      Mol. Cell. Neurosci. 7:289-303(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=97183663;
RA      Ninkina N.N., Baka I.D., Buchman V.L.;
RT      "Rat and chicken s-rex/NSP mRNA: nucleotide sequence of main
RT      transcripts and expression of splice variants in rat tissues.";
RL      Gene 184:205-210(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; U17606; AAC60075.1; -.
DR      EMBL; AY164724; AAP47301.1; -.
DR      GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      760 AA;      82502 MW;      465C1B429F799D5C CRC64;

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Query Match          13.3%;  Score 788.5;  DB 13;  Length 760;
Best Local Similarity 27.7%;  Pred. No. 7e-31;
Matches 296;  Conservative 115;  Mismatches 315;  Indels 341;  Gaps 38;

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Qy 143 PPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNT 202  
 || | : | | | | | : |  
 Db 4 PPDPQDLLLAGTAER-W-----AAAGADEYAAGAALRDGDGA-----QOREQL 45

Qy 203 ISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEV 262  
 : | | : || | | : : | : | : : |  
 Db 46 AFGSAREHPPVAMATA-----SPGVTASSRLFDY-----GSSSANGADSSFYT 88

Qy 263 SEKAKTLLID-----RDLTEFSELEYSEMSSFSVSPKAESAVIVANPREEIIVKNKDE 316  
 | : | | | : : | : | : : | : : |  
 Db 89 S-----LISDVHYTTPRDNTYFTGV-YQQENSPIPCSGSTEGFNALGHPVQDV---TGFE 139

Qy 317 EEKLVSNNILHXQQELPTALTCLKVEDEVSSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376  
 | | | : : | | : : | : | :  
 Db 140 SRGLFS-----LDSGIEMTPAESAE-----EVDKSLTDPMKVEGYKYMDI 178

Qy 377 ERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSSESSNDD--TSFP 434  
 | : | | : | | : | : | :  
 Db 179 SRPEEIK-----YQEKHDPDSEDESPDLIDEYR 206

Qy 435 STPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKQIVTEK 494  
 || | | : : | : | : : | : : | : ||  
 Db 207 GTPIG----SGH--AAEPQRTTASEAIIKA--PKEQDPLE----DKSFRDQHNASVVTAP 253

Qy 495 NTSTKTSNPFVAAQDSETDYVTTDNLTKEVEEVVANM---PE-----GLTP 538  
 | | | | : : | : | : | : | :  
 Db 254 VKITLTETPGAREATSKEASVTQPKSGLKPSHEVVPTVMVSEPDDSPGSVTPPSSGTEP 313

Qy 539 DLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFEESEATPSPVLP 598  
 : : | : | | : | | : | | : | : |  
 Db 314 SGSESQKGKSLSEDELISAIKEAKGFSFETSEVQQS---PAV---SAEKQEQQMKMPGRP 366

Qy 599 DIVMEAPLNSAVPSA--GASVIQ-PSSSPLEASSV---NYESIKHEPENPPPYEEAMSVS 652  
 : : | : : | | | : | | | | : | : | : |  
 Db 367 --AVPSPLDNEASSAESGDSEIELVSEDPLAAEEVLHSNYMTFSH-IGGPPP--SPASPS 421

Qy 653 LKVSGIKKEEIKPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQP 712  
 : : | : : | : : | : | : : | : | : | : |  
 Db 422 IQYSILREERE-----AELDSELIIESCD----ASSASEESP-----KREQD 459

Qy 713 VPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLESILTETSFESMIEYENKEK 772  
 | : | : : | : : | : : | : :  
 Db 460 SPLMKPMVMD-----IIEK-----ENSSR 478

Qy 773 LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI 832  
 || |  
 Db 479 ASASDYE----- 485

Qy 833 SKEAQIRETETTFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA 892  
 : || | : : | : | : | : |  
 Db 486 -----ASKTTE-SRMNRE-----NLADSA 503

Qy 893 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIES 952  
 | : : | : : | : : | : :  
 Db 504 SYLKSS-----FVAPKVSS-----PPTSASVSTEELKERI 533

Qy	953	IVKPKVLEKEAEKKLPDTEKEDRSPSAI-FSADLGKTSVVDLLYWRDIKKTGVVFGASL	1011
Db	534	ILKKPIEETVVNQSKVSSKDSGKRSPALPLLPFLNKQKAINLLYWRDIKQTGIVFGSL	593
Qy	1012	FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISE	1071
Db	594	LLLSLTVFSIVSVVAYLALAGLSATISFRIYKSVLQAVQKTDEGHPFKAYLDMEMNLSQ	653
Qy	1072	ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL	1131
Db	654	DQIQKYTDCLQLYVNSTVKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLIMAV	713
Qy	1132	ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	714	VSMFTLPVVYDKYQAQIDQYLGLVRTHINTVVAKIQAKIPGAKRKAE	760

Search completed: September 3, 2004, 16:08:53  
Job time : 82.0403 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:58:54 ; Search time 15.6624 Seconds  
(without alignments)  
3916.307 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
		Query					
Result	No.	Score	Match	Length	DB	ID	Description
1	5815	98.2	1192	1	RTN4_HUMAN	Q9nqc3	homo sapien
2	4296.5	72.5	1163	1	RTN4_RAT	Q9jkl1	rattus norv
3	915	15.4	199	1	RTN4_MOUSE	Q99p72	mus musculu
4	791	13.4	777	1	RTN1_RAT	Q64548	rattus norv
5	787.5	13.3	776	1	RTN1_HUMAN	Q16799	homo sapien
6	626	10.6	237	1	RTN3_MOUSE	Q9es97	mus musculu
7	625.5	10.6	236	1	RTN3_HUMAN	O95197	homo sapien
8	514	8.7	545	1	RTN2_HUMAN	O75298	homo sapien
9	500	8.4	471	1	RTN2_MOUSE	O70622	mus musculu
10	324.5	5.5	865	1	CPN_DROME	Q02910	drosophila
11	320	5.4	5147	1	PCLO_HUMAN	Q9y6v0	homo sapien
12	315	5.3	5038	1	PCLO_MOUSE	Q9qyx7	mus musculu
13	299	5.0	3924	1	ANK2_HUMAN	Q01484	homo sapien
14	296.5	5.0	2468	1	MAPB_HUMAN	P46821	homo sapien
15	289	4.9	2459	1	MAPB_RAT	P15205	rattus norv
16	289	4.9	2464	1	MAPB_MOUSE	P14873	mus musculu
17	287	4.8	5120	1	PCLO_CHICK	Q9pu36	gallus gall



18	286.5	4.8	3644	1	MINT_MOUSE	Q62504	mus musculu
19	276	4.7	5085	1	PCLO_RAT	Q9jks6	rattus norv
20	273.5	4.6	3664	1	MINT_HUMAN	Q96t58	homo sapien
21	264.5	4.5	8545	1	ANCL1_CAEEL	Q9n4m4	caenorhabdi
22	263.5	4.4	3396	1	PGCV_HUMAN	P13611	homo sapien
23	262.5	4.4	6632	1	UN89_CAEEL	O01761	caenorhabdi
24	260.5	4.4	3381	1	PGCV_BOVIN	P81282	bos taurus
25	259.5	4.4	1828	1	MAP2_MOUSE	P20357	mus musculu
26	258.5	4.4	2805	1	MAPA_HUMAN	P78559	homo sapien
27	258	4.4	1616	1	P200_MYCGE	Q49429	mycoplasma
28	257.5	4.3	1781	1	AK12_HUMAN	Q02952	homo sapien
29	257.5	4.3	2738	1	PGCV_RAT	Q9erb4	rattus norv
30	253	4.3	1189	1	YJH6_YEAST	P47035	saccharomyc
31	252	4.3	4377	1	ANK3_HUMAN	Q12955	homo sapien
32	250.5	4.2	1861	1	MAP2_RAT	P15146	rattus norv
33	249.5	4.2	1827	1	MAP2_HUMAN	P11137	homo sapien
34	248	4.2	3421	1	TEGU_HSVEB	P28955	equine herp
35	244	4.1	1362	1	BRD4_HUMAN	O60885	homo sapien
36	242	4.1	1790	1	USO1_YEAST	P25386	saccharomyc
37	239	4.0	1744	1	TANA_XENLA	Q01550	xenopus lae
38	238.5	4.0	1411	1	TCOF_HUMAN	Q13428	homo sapien
39	236.5	4.0	3358	1	PGCV_MOUSE	Q62059	mus musculu
40	235.5	4.0	1723	1	AIM1_HUMAN	Q9y4k1	homo sapien
41	233.5	3.9	1087	1	NFH_MOUSE	P19246	mus musculu
42	232	3.9	1140	1	YM96_YEAST	Q04893	saccharomyc
43	231	3.9	3256	1	KI67_HUMAN	P46013	homo sapien
44	229.5	3.9	1367	1	AMYPH_YEAST	P08640	saccharomyc
45	228.5	3.9	1306	1	MSB2_YEAST	P32334	saccharomyc

#### ALIGNMENTS

##### RESULT 1

RTN4\_HUMAN

ID RTN4\_HUMAN STANDARD; PRT; 1192 AA.

AC Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;

AC Q9Y5U6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific

DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).

GN RTN4 OR NOGO OR ASY OR KIAA0886.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129242; PubMed=10667780;

RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,

RA Michalovich D., Simmons D.L., Walsh F.S.;

RT "Inhibitor of neurite outgrowth in humans.";

RL Nature 403:383-384(2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=21010696; PubMed=11126360;  
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";  
 RL Oncogene 19:5736-5746(2000).  
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20237542; PubMed=10773680;  
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
 RT 2p14-->2p13 by radiation hybrid mapping.";  
 RL Cytogenet. Cell Genet. 88:101-102(2000).  
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RA Jin W.-L., Ju G.;  
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Placenta, and Skeletal muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in human.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Fibroblast;  
 RA Yutsudo M.;  
 RT "Isolation of a cell death-inducing gene.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Pituitary;  
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
 RA Luo B., Hu R., Chen J.;  
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel human cDNA clone with function of inhibiting cancer cell  
 RT growth.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:355-364(1998).  
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RX MEDLINE=20499367; PubMed=11042152;  
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [12]  
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
 RC TISSUE=Brain;  
 RA Mao Y.M., Xie Y., Zheng Z.H.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [13]  
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Testis;  
 RA Sha J.H., Zhou Z.M., Li J.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [14]  
 RP TOPOLOGY.  
 RC TISSUE=Brain;  
 RX MEDLINE=20129259; PubMed=10667797;  
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
 RT "Identification of the Nogo inhibitor of axon regeneration as a  
 RT Reticulon protein.";  
 RL Nature 403:439-444(2000).  
 RN [15]  
 RP FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=21069055; PubMed=11201742;  
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;  
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";  
 RL Nature 409:341-346(2001).  
 RN [16]  
 RP REVIEW.  
 RX MEDLINE=21888956; PubMed=11891768;  
 RA Ng C.E.L., Tang B.L.;  
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron  
 RT regeneration.";  
 RL J. Neurosci. Res. 67:559-565(2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults.  
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.  
 CC This is likely consecutive to their change in subcellular  
 CC location, from the mitochondria to the endoplasmic reticulum,  
 CC after binding and sequestration.  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
 CC through 2 putative transmembrane domains.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;  
 CC IsoId=Q9NQC3-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;  
 CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;  
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;  
 CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
 CC Name=4;  
 CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
 CC widely expressed excepted for the liver. Isoform 3 is expressed in  
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
 CC specific.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
 CC frameshifts in positions 1149 and 1156.

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 CC -----

DR EMBL; AJ251383; CAB99248.1; -.  
 DR EMBL; AJ251384; CAB99249.1; -.  
 DR EMBL; AJ251385; CAB99250.1; -.  
 DR EMBL; AB040462; BAB18927.1; -.  
 DR EMBL; AB040463; BAB18928.1; -.  
 DR EMBL; AF148537; AAG12176.1; -.  
 DR EMBL; AF148538; AAG12177.1; -.  
 DR EMBL; AF087901; AAG12205.1; -.  
 DR EMBL; AF320999; AAG40878.1; -.  
 DR EMBL; AF132047; AAD31021.1; -.  
 DR EMBL; AF132048; AAD31022.1; -.





RL Biochim. Biophys. Acta 1450:68-76(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20129258; PubMed=10667796;  
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
 RA Spillmann A.A., Christ F., Schwab M.E.;  
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
 RT antigen for monoclonal antibody IN-1.";  
 RL Nature 403:434-439(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in rat: one of two  
 RT minor splice variants.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=22033691; PubMed=12037567;  
 RA GrandPre T., Li S., Strittmatter S.M.;  
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
 RL Nature 417:547-551(2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
 CC membrane of the endoplasmic reticulum through 2 putative  
 CC transmembrane domains (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Nogo-A, NI-220-250;  
 CC IsoId=Q9JK11-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;  
 CC IsoId=Q9JK11-2; Sequence=VSP\_005658;  
 CC Name=3; Synonyms=Nogo-C, VP20;  
 CC IsoId=Q9JK11-3; Sequence=VSP\_005656, VSP\_005657;  
 CC Name=4; Synonyms=Foocen-M2;  
 CC IsoId=Q9JK11-4; Sequence=VSP\_005659;  
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic  
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are  
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells  
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,  
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high  
 CC level in skeletal muscle. In adult animals isoform 1 is expressed  
 CC mainly in the nervous system.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
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 CC -----

DR EMBL; AF051335; AAF01564.1; -.  
 DR EMBL; AJ242961; CAB71027.1; -.  
 DR EMBL; AJ242962; CAB71028.1; -.  
 DR EMBL; AJ242963; CAB71029.1; -.  
 DR EMBL; AF132045; AAD31019.1; -.  
 DR EMBL; AF132046; AAD31020.1; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.  
 DR GO; GO:0005635; C:nuclear membrane; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.  
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).  
 FT TRANSMEM 990 1010 POTENTIAL.  
 FT DOMAIN 1011 1104 LUMENAL (Potential).  
 FT TRANSMEM 1105 1125 POTENTIAL.  
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).  
 FT DOMAIN 976 1163 RETICULON.  
 FT DOMAIN 33 46 POLY-GLU.  
 FT DOMAIN 73 76 POLY-ALA.  
 FT DOMAIN 140 145 POLY-PRO.  
 FT VARSPLIC 1 964 Missing (in isoform 3).  
 FT /FTId=VSP\_005656.  
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).  
 FT /FTId=VSP\_005657.  
 FT VARSPLIC 173 975 Missing (in isoform 2).  
 FT /FTId=VSP\_005658.  
 FT VARSPLIC 192 975 Missing (in isoform 4).  
 FT /FTId=VSP\_005659.  
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).  
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 72.5%; Score 4296.5; DB 1; Length 1163;  
 Best Local Similarity 74.0%; Pred. No. 2e-157;  
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58  
 |||:|||| ||||| ||||| ||||| ||||| |||||:|:|||||||  
 Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEEDDEEEDDEDLEELEVLERK 60  
 Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118  
 ||||| || ||| |||:| :| ||||| ||||| |||||: || : |  
 Db 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA--P 115  
 Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178  
 ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166  
 Qy 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224  
 ||| : ||||| |||||:|:||||||| ||||| |||||  
 Db 167 RGSGSVDETLFALPAASEVPVPSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226  
 Qy 225 SPLSAAAFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284



Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSTRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKKAIIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLT	523
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPPFLVAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSGIKEEIKPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIQEVQQTQEEAVMLKESLTVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTDSSFKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESETFSDDSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVS	942
Db	871	SEIANIQSGADSLPCLLPCLDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMVFTYVGFALFN	1122

Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||:||||| |||||:|||||

Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

# RESULT 3

## RTN4\_MOUSE

ID RTN4\_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).

GN RTN4 OR NOGO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3T3-L1; TISSUE=Adipocyte;

RA Coulson A.C., Craggs P.D., Morris N.J.;

RT "Mouse vp20/RTN4C cDNA.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 170-199 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults (By

CC similarity).

CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By

CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the

CC membrane of the endoplasmic reticulum through 2 putative



RESULT 4

RTN1\_RAT

ID RTN1\_RAT STANDARD; PRT; 777 AA.  
AC Q64548; Q64547;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).  
GN RTN1 OR NSP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).  
RC STRAIN=Wistar; TISSUE=Brain cortex;  
RX MEDLINE=96386034; PubMed=8793864;  
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,  
RA Georgiev G.P., Buchman V.L.;  
RT "Intracellular compartmentalization of two differentially spliced s-  
RT rex/NSP mRNAs in neurons."  
RL Mol. Cell. Neurosci. 7:289-303(1996).  
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in  
CC membrane trafficking in neuroendocrine cells.  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By  
CC similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=RTN1-B; Synonyms=S-RexB;  
CC IsoId=Q64548-1; Sequence=Displayed;  
CC Name=RTN1-S; Synonyms=S-RexS;  
CC IsoId=Q64548-2; Sequence=VSP\_005647, VSP\_005648;  
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND  
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS  
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.  
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL  
CC TYPES.  
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE  
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC  
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN  
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB  
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE  
CC HINDBRAIN.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
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CC -----  
DR EMBL; U17604; AAC53046.1; -.  
DR EMBL; U17603; AAC53045.1; -.

DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
 FT TRANSMEM 604 624 POTENTIAL.  
 FT TRANSMEM 727 747 POTENTIAL.  
 FT DOMAIN 590 777 RETICULON.  
 FT DOMAIN 610 613 POLY-LEU.  
 FT VARSPLIC 1 569 Missing (in isoform RTN1-S).  
 FT /FTid=VSP\_005647.  
 FT VARSPLIC 570 589 IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW  
 FT KSQ (in isoform RTN1-S).  
 FT /FTid=VSP\_005648.  
 SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

Query Match 13.4%; Score 791; DB 1; Length 777;  
 Best Local Similarity 26.6%; Pred. No. 1.4e-23;  
 Matches 290; Conservative 129; Mismatches 308; Indels 364; Gaps 39;

Qy 134 PEDDEPPARPPPPPPASVSPQAE-PVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKI 192  
 |: : | | | : | || || || |: ||  
 Db 5 PDLQDEPLSPANPGSQLFGGRGEGEEATPKGARPAQQDGEPAWGS--GAGAGVVS----- 57

Qy 193 MDLKEQPGNTISAGQEDFPSVLLETA----ASXP-SLSPLSAASFKEHE---YLGNLSTV 244  
 : : | | | : || | : | : | : | : | :  
 Db 58 -----SRGLCSGPARSPPVAMETASTGVAAPDALDHSSSPTLKDGEGACYTSLISDI 110

Qy 245 L--PTE-----GTLQE-----NVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFS 291  
 | | | ||: ||: :|: : | : | | : | :  
 Db 111 CYPPREDSAYFTGILQKENGHITTSESPEELGTPGPS-LPEVPGTEPHGLLSDDSGIEMT 169

Qy 292 VSPKAESAVIVANPREELIIVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKA 351  
 : | | :|:| : :  
 Db 170 PAESTEVENKILADPLDQ----- 186

Qy 352 KDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCF 411  
 |: | : | | | :| | |  
 Db 187 -----MKAEEACKYIDITRQEAQGEQSPGL----- 213

Qy 412 ADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATES--IATNIFPLL 469  
 :|| : : |: : |||: || |: | | |:|  
 Db 214 -----EDKDLDFKDKDSEVSTKPEGVH-----APNQPSPEVGKLIKDNLF--- 253

Qy 470 EDPTSENXTDEKKIEEKKAQIVTE--KNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527  
 |: | || |: : :|| | | |: | | : :  
 Db 254 EESTFAPYIDELSDEQHRMSLVTAPVKITLTEIGPPVMTATHET----- 297

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFE 587  
 :|| | || | |: | :  
 Db 298 ----IPE-----KQDL-----CLKPSPDTPVPTVT 317

Qy 588 ESEA---TPSPVLPDIVMEAPLNSAVPSAGASVIQSSSP-----LEASSVNYESIKH 637  
 || :| | | : ||| | : | | || :||:  
 Db 318 VSEPEDDSPGSVT-----PSSGTEPSAAESQKGKSVSEDELIAAIKEAKGLSYET--- 368

Qy 638 EPENPPPYEEAMSVSLKVGSIKEEIKE-----PENINAALQETEAPYISIIACDLIKET 690  
 |: | :| : :| | : : | : | :|: |

Db 369 -TESPRPVGQAAD-----RPKVKARSGLPPTIPSSLDQEASSAESGDSEI--ELVSED 417  
 QY 691 KLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQVDPQKQDETVM 750  
 : : | | | | | | | | | | | | | | | | : :  
 Db 418 PMASEDALP-SGYVSFGHVS GPPP-----SPAS-----PSIQYSILREEREAE 459  
 QY 751 LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK 810  
 | | : | : | : : | | | : | : : | : : :  
 Db 460 LDSELIIESCDASSASEESPKREQDSPPM--KPGV-----LD-----AIREETSSRATE 506  
 QY 811 EKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSPIE---IIDEFPTLISSKTDSF 867  
 | : | | : | | : | : | : | : :  
 Db 507 ERAP-----SHQGPVEPDPILSFTPTLQSRPE-- 534  
 QY 868 SKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNG 927  
 | | | | | | | : | | | | : | : :  
 Db 535 -----PSSGDGAPVPEPP-----KSQQQKPEEEAVSS---SQSP 565  
 QY 928 SATSKVLLLPPDV SALGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLG 987  
 : | | : : | : | : | :  
 Db 566 AAT-----EIPGPLGSDLV PPLPFFN----- 586  
 QY 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK GVI 1047  
 | : | | | | | | : | | | : | | | | : | | | | | :  
 Db 587 KQKAIDL LLYWRDIKQTGIVFGSFLLLLSLTQFSVVSVVAYLALALASATISFRIYKSVL 646  
 QY 1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKF 1107  
 | : | : | | | | : | | | : : | : : | : | : | : | : | : | : | : | : | : | :  
 Db 647 QAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKE LRRLFLVQDLVDSLKF 706  
 QY 1108 AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167  
 | | | | : | | | | | | | | : : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 707 AVLMWLLTYVGALFNGLTLLLLMAVVSMTFLPVVYVKHQAQVDQYLG LVRTHINTVVAKIQ 766  
 QY 1168 AKIPGLKRKAE 1178  
 | | | | | | | |  
 Db 767 AKIPGAKRHAE 777

# RESULT 5

## RTN1\_HUMAN

ID RTN1\_HUMAN STANDARD; PRT; 776 AA.  
 AC Q16799; Q16800; Q16801;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Reticulon 1 (Neuroendocrine-specific protein).  
 GN RTN1 OR NSP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).  
 RC TISSUE=Lung carcinoma;  
 RX MEDLINE=93293865; PubMed=7685762;  
 RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,

RA Ramaekers F.C.S., Van de Ven W.J.M.;  
 RT "Cloning and expression of alternative transcripts of a novel  
 RT neuroendocrine-specific gene and identification of its 135-kDa  
 RT translational product.";  
 RL J. Biol. Chem. 268:13439-13447(1993).  
 RN [2]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=96429995; PubMed=8833145;  
 RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,  
 RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;  
 RT "Genomic organization of the human NSP gene, prototype of a novel gene  
 RT family encoding reticulons.";  
 RL Genomics 32:191-199(1996).  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=98228245; PubMed=9560466;  
 RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,  
 RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;  
 RT "Neuronal differentiation is accompanied by NSP-C expression.";  
 RL Cell Tissue Res. 292:229-237(1998).  
 CC -!- FUNCTION: May be involved in neuroendocrine secretion or in  
 CC membrane trafficking in neuroendocrine cells.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=RTN1-A; Synonyms=NSP-A;  
 CC IsoId=Q16799-1; Sequence=Displayed;  
 CC Name=RTN1-B; Synonyms=NSP-B;  
 CC IsoId=Q16799-2; Sequence=VSP\_005644;  
 CC Name=RTN1-C; Synonyms=NSP-C;  
 CC IsoId=Q16799-3; Sequence=VSP\_005645, VSP\_005646;  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES  
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C  
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.  
 CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; L10333; AAA59950.1; -.  
 DR EMBL; L10334; AAA59951.1; -.  
 DR EMBL; L10335; AAA59952.1; -.  
 DR PIR; A46583; A46583.  
 DR PIR; I60904; I60904.  
 DR Genew; HGNC:10467; RTN1.  
 DR MIM; 600865; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.  
 DR GO; GO:0004871; F:signal transducer activity; NAS.  
 DR GO; GO:0030182; P:neuron differentiation; TAS.  
 DR GO; GO:0007165; P:signal transduction; NAS.  
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Phosphorylation.  
 FT TRANSMEM 603 623 POTENTIAL.  
 FT TRANSMEM 726 746 POTENTIAL.  
 FT DOMAIN 589 776 RETICULON.  
 FT DOMAIN 609 612 POLY-LEU.  
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).  
 FT /FTId=VSP\_005644.  
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).  
 FT /FTId=VSP\_005645.  
 FT VARSPLIC 569 588 GPGPLGPGAPPPLFLNKQK -> MQATADSTKMDCVWSNW  
 FT KSQ (in isoform RTN1-C).  
 FT /FTId=VSP\_005646.  
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 13.3%; Score 787.5; DB 1; Length 776;  
 Best Local Similarity 31.9%; Pred. No. 2e-23;  
 Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

Qy 588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY---- 632  
 | ||| ||| : | | : | : | : | : | : |  
 Db 141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDIT 200  
 Qy 633 --ESIKHEPENPPPYEEA-----MSVSLKVSGIKEEIKEPENINAAL-----QET 675  
 | : || : :: | | : : || | | : | : : |  
 Db 201 RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST 259  
 Qy 676 EAPYISIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPVDHSELVED 722  
 |||| || : | | || : : : | : : :  
 Db 260 FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309  
 Qy 723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF 761  
 ||| : | | || | : | || : : || :  
 Db 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA----- 363  
 Qy 762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821  
 : || | : : | : || | || : : :  
 Db 364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403  
 Qy 822 TAVYSNDDLFISKEAQIRETETFSDSPIEIIIDFP---TLISSKTDSFS----- 868  
 : : | | | || : | | : | ||  
 Db 404 SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP 444  
 Qy 869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921  
 : || : | : : | : : | : | | | |  
 Db 445 ASPSIQYSILREEREAEELDELIIESCDASSAS-----EESPKREQDSPPMKPSALD 496  
 Qy 922 DF-----SKNGSATSKVLL-----LPPDVSA LGHTQAEIESIVKP 956  
 | : | | | || | | | : : |  
 Db 497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGAL-----EPETPMLP 551  
 Qy 957 KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001  
 : | : : : || : | | : |||||  
 Db 552 -----RKPEEDSSSNQSPAATKGGPLGPGAPPPLLF--LNKQKAIDL YWRDIK 599





CC       reticulum (Potential).  
 CC    -!- SIMILARITY: Contains 1 reticulon domain.  
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 CC    -----  
 DR    EMBL; AF195940; AAG31360.1; -.  
 DR    EMBL; BC014697; AAH14697.1; -.  
 DR    MGD; MGI:1339970; Rtn3.  
 DR    InterPro; IPR003388; Reticulon.  
 DR    Pfam; PF02453; Reticulon; 1.  
 DR    PROSITE; PS50845; RETICULON; 1.  
 KW    Transmembrane; Endoplasmic reticulum.  
 FT    TRANSMEM       69       89       POTENTIAL.  
 FT    TRANSMEM       167      187      POTENTIAL.  
 FT    DOMAIN        49       237      RETICULON.  
 SQ    SEQUENCE       237 AA;   25428 MW;   EB60A0A7AC45F0DE CRC64;

Query Match                   10.6%;   Score 626;   DB 1;   Length 237;  
 Best Local Similarity       53.2%;   Pred. No. 6.9e-18;  
 Matches 125;   Conservative   41;   Mismatches   53;   Indels    16;   Gaps     4;

QY       960 EKEAEKKLPS-DTEKEDRSPSAIFSAD-----LGKTS-----VVDLLYWRDIKKTG 1004  
           | | : || :       |||:               || |       | ||: |||: ||||  
 Db       3 ESSAATQSPSVSSSSSGAEPALGGGGGSPGACPALGAKSCGSSCAVHDLIFWRDVKKTG 62  
 QY       1005 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLE 1064  
           ||| :| : |||| ||::|| :| : ||||| |||||: || ||||: |||: |||||: |||:  
 Db       63 FVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSVIQAVQKSEEGHPFKAYLD 122  
 QY       1065 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFETYVGALENGL 1124  
           :: :| |   | |:|: ||| :| : |||||: ||||| || ||: |||||: |||:  
 Db       123 VDTLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGAVFNGI 182  
 QY       1125 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKA 1178  
           ||||| : : ||||: |||:: |||||: |||   | : |||||: ||| : |||  
 Db       183 TLLILAELLVFSVPVIEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIKAKKAE 237

# RESULT 7

## RTN3\_HUMAN

ID   RTN3\_HUMAN       STANDARD;       PRT;   236 AA.  
 AC   095197;  
 DT   16-OCT-2001 (Rel. 40, Created)  
 DT   16-OCT-2001 (Rel. 40, Last sequence update)  
 DT   10-OCT-2003 (Rel. 42, Last annotation update)  
 DE   Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like  
 DE   protein II) (NSPLII).  
 GN   RTN3 OR NSPL2.  
 OS   Homo sapiens (Human).  
 OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Retina;  
 RX MEDLINE=99265974; PubMed=10331947;  
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;  
 RT "Cloning of a novel member of the reticulon gene family (RTN3): gene  
 RT structure and chromosomal localization to 11q13.";  
 RL Genomics 58:73-81(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;  
 RT "Cloning and expression analysis of a cDNA encoding a novel  
 RT neuroendocrine-specific protein-like protein 1: NSPL1.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Eye, and Lymph;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN  
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL  
 CC RETINA.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF059524; AAC99319.1; -.  
 DR EMBL; AF059529; AAD20951.1; -.  
 DR EMBL; AF059525; AAD20951.1; JOINED.

DR EMBL; AF059526; AAD20951.1; JOINED.  
 DR EMBL; AF059527; AAD20951.1; JOINED.  
 DR EMBL; AF059528; AAD20951.1; JOINED.  
 DR EMBL; AF119297; AAD26810.1; -.  
 DR EMBL; BC000634; AAH00634.1; -.  
 DR EMBL; BC010556; AAH10556.1; -.  
 DR EMBL; BC011394; AAH11394.1; -.  
 DR EMBL; BC022993; AAH22993.1; -.  
 DR Genew; HGNC:10469; RTN3.  
 DR MIM; 604249; -.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Transmembrane; Endoplasmic reticulum.  
 FT TRANSMEM 68 88 POTENTIAL.  
 FT TRANSMEM 177 197 POTENTIAL.  
 FT DOMAIN 48 236 RETICULON.  
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCD7B7 CRC64;

Query Match 10.6%; Score 625.5; DB 1; Length 236;  
 Best Local Similarity 54.8%; Pred. No. 7.1e-18;  
 Matches 119; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

Qy 963 AEKKLPSTEDKEDRSPSAIFSAIDLKGTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022  
 || | : : : ||::||:|||| ||| :| :||| ||:  
 Db 20 AEPSAPGGGGSPGACPALGTKSCSSSCAVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSV 79  
 Qy 1023 VSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSAL 1082  
 :|| :|: ||||| ||||| ||||:||||: ||: :| | | :|:  
 Db 80 ISVVSYLILALLSVTISFRIYKSVIAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139  
 Qy 1083 GHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYE 1142  
 |:| :| : ||||:||||| || ||: ||||:||||: ||||| : :|||:|:  
 Db 140 VHINRALKLIIRLFLVEDLVDLSLKLAVFMWLMFTYVGAVFNGITLLILAEELLIFSVPIVYE 199  
 Qy 1143 RHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178  
 ::: ||||:|:| | : ||||:|:| | :|||  
 Db 200 KYKTQIDHYVGIARDQTKSIVEKIQAKLPGIKKAE 236

# RESULT 8

## RTN2\_HUMAN

ID RTN2\_HUMAN STANDARD; PRT; 545 AA.  
 AC O75298; O60509;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

RC TISSUE=Lung carcinoma;  
 RX MEDLINE=98360096; PubMed=9693037;  
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;  
 RT "cDNA cloning, genomic organization, and expression of the human RTN2  
 RT gene, a member of a gene family encoding reticulons.";  
 RL Genomics 51:98-106(1998).  
 RN [2]  
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).  
 RC TISSUE=Brain;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 RT neural expression.";  
 RL Mamm. Genome 9:274-282(1998).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=RTN2-A;  
 CC IsoId=O75298-1; Sequence=Displayed;  
 CC Note=Isoform RTN2-C is produced by alternative initiation at  
 CC Met-341 of isoform RTN2-A;  
 CC Name=RTN2-B;  
 CC IsoId=O75298-2; Sequence=VSP\_005649;  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced  
 CC by alternative initiation at Met-1 and Met-341;  
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL  
 CC MUSCLE.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF004222; AAC32542.1; -.  
 DR EMBL; AF004223; AAC32543.1; -.  
 DR EMBL; AF004224; AAC32544.1; -.  
 DR EMBL; AF038540; AAC14910.1; -.  
 DR Genew; HGNC:10468; RTN2.  
 DR MIM; 603183; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.  
 DR GO; GO:0004871; F:signal transducer activity; NAS.  
 DR GO; GO:0007165; P:signal transduction; NAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Alternative initiation.  
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.  
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.  
 FT INIT\_MET 341 341 FOR ISOFORM RTN2-C.  
 FT TRANSMEM 368 388 POTENTIAL.

FT TRANSMEM 463 483 POTENTIAL.  
 FT DOMAIN 345 545 RETICULON.  
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).  
 FT /FTId=VSP\_005649.  
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 8.7%; Score 514; DB 1; Length 545;  
 Best Local Similarity 28.2%; Pred. No. 3.7e-13;  
 Matches 169; Conservative 81; Mismatches 186; Indels 164; Gaps 18;

Qy 676 EAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPD-SEPVDL-F 733  
 ||| | | | | | : : : | | : | | : | |  
 Db 13 EAP-----STASSTPDSTEGNDDSDFRELHTAREFSEEDDEE--ETTSQDWGTPRELTF 64  
 Qy 734 S-----DDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG 780  
 | | | | | : | : | : | : | : | | |  
 Db 65 SYIAFDGVVGSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGDLSLESIPSLSQSPEPGRR 124  
 Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840  
 | | | | | | | | : | : : | : : : |  
 Db 125 GDP-----DTAPPSE----RPLEDLRLRLDHLG-----WVARGTGSGE 158  
 Qy 841 TETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900  
 : | | : | : | | | : | | | | | | |  
 Db 159 DSSTSSSTPLE--DEEP-----QEPNRLETGEAGE-----EL 188  
 Qy 901 PHDLSLKNIQPKVEEKI-----SFSDDFSKNGSATS KVL LPPDV SALGHT 946  
 | | | : | | | : : | | : : : | | : |  
 Db 189 --DLRLRLAQPS SPEVLTPQLSPGSGTPQAGTPSPSRSDSNSGPPEEPLLEEEEEKQWGPL 246  
 Qy 947 QAE-----IESIVKPKVLEKEAE-----KKLP----- 968  
 : | : | | : | : | : | : | : | : |  
 Db 247 EREPVRGQCLDSTDQLEFTVEPRLLGTAMEWLKTSLLLAVYKTVPILELSPPLWTAIGWV 306  
 Qy 969 -----SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASL 1011  
 : : : | | | : | | | : | : | : | :  
 Db 307 QRGPTPPTPVLRVLLKWAKSPRSSGVPSLSLGADMG-SKVADLLYWKDTRTSGVVFTGLM 365  
 Qy 1012 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071  
 | | | | | | | | : : | | | | | : : | : | : | : : :  
 Db 366 VSLCLLHFSIVSVA AHLALLLLCGTISLRVYRKVLQAVHRGDGANPFQAYLDVDLTLTR 425  
 Qy 1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVIMMWVFTYVGALENGLTLLILAL 1131  
 | : : | : | : | | | : | | | : | : | : | : | : | : | :  
 Db 426 EQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALLFYILTFVGAIENGLTLLILGV 485  
 Qy 1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-----KRKAE 1178  
 | | : : | : : | | | | | : | : | : | : | : | : |  
 Db 486 IGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAA VSGSKAKAE 545

RESULT 9

RTN2\_MOUSE

ID RTN2\_MOUSE STANDARD; PRT; 471 AA.

AC 070622; 070620;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like  
 DE protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 RT neural expression."  
 RL Mamm. Genome 9:274-282(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Retina;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum  
 CC (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Brain;  
 CC IsoId=O70622-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Muscle;  
 CC IsoId=O70622-2; Sequence=VSP\_005650, VSP\_005651;  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular  
 CC tissues.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.

CC -----  
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CC -----

DR EMBL; AF038537; AAC14906.1; -.  
DR EMBL; AF038537; AAC14907.1; -.  
DR EMBL; AF038538; AAC14908.1; -.  
DR EMBL; AF038539; AAC14909.1; -.  
DR EMBL; AF093624; AAD13195.1; -.  
DR EMBL; BC031370; AAH31370.1; -.  
DR MGD; MGI:107612; Rtn2.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
FT TRANSMEM 295 315 POTENTIAL.  
FT DOMAIN 272 471 RETICULON.  
FT VARSPLIC 1 267 Missing (in isoform 2).  
FT /FTid=VSP\_005650.  
FT VARSPLIC 268 271 PLLL -> MGSK (in isoform 2).  
FT /FTid=VSP\_005651.  
SQ SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

Query Match 8.4%; Score 500; DB 1; Length 471;  
Best Local Similarity 29.3%; Pred. No. 1.1e-12;  
Matches 159; Conservative 83; Mismatches 177; Indels 124; Gaps 16;

Qy 676 EAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPD-SEPVDL-F 733  
||| | | | | | : | | | : | |  
Db 13 EAP-----STASSTPDSTEGNDDSDFRELHTAREFSEDEEE--ETTSQDWGTPRELTF 64  
  
Qy 734 S-----DDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG 780  
| ||: | : | : : : | |  
Db 65 SYIAFDGVVGSGGRRDSVVRPRPQGRSVSEPRDPPQQSGLGDSLESIPSLSQSPEPGRR 124  
  
Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRE 840  
| | | : | | | : | : : | : : | |  
Db 125 GDP-----DPVPPAE----RPLEELRLRLDQLG-----WVVR SAGSGE 158  
  
Qy 841 TETFS DSSPIEIIDEFPTLISS-----KTDSF SKLARE-YTDLEV-----SHKSEIAN 887  
| | : | : | : : : : | : | : | : | :  
Db 159 DSATSSSTPLE--NEEPD GLEA SEAGEETNLELRLAQSLHLQLEVLTPQLSPSSGTPQAH 216  
  
Qy 888 APDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV S ALGHTQ 947  
| | | | | : | | : : | | : : | : :  
Db 217 TPSPQRSQDSNSGPDDEPLLN V--VEEH-----WRLLEQEPITAQCLDST 259  
  
Qy 948 AEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF S ADLGKTSVVDLLYWRDIKKTGVVF 1007  
: | : : | : | | | | : | : | : |  
Db 260 DQSEFMLEPLLL-----VADLLYWKDTRTSGAVF 288  
  
Qy 1008 GASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHFPFRAYLESEV 1067  
: | | | | | | : : | | | : : | : : | : :  
Db 289 TGLMASLLCLLHFSIVSVA AHLALLGLCATISLRVYRKVLQAVHRGDGTNP FQAYLDMDL 348  
  
Qy 1068 AISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVFLMWVFTYVGALFNGLTLL 1127  
: : | : : | | | : | | | : | : | : | : | :  
Db 349 TLTREQTERLSQQIASHVVSTATQLRHFFLVEDLVDSLKLALLFYILTFVGAIFNGLTLV 408



QY 1128 ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-----KR 1175  
 || ::||:|:|:| :||| | :| | :|:| | |  
 Db 409 ILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGTLAPTASVSGSKA 468

QY 1176 KAE 1178  
 |||  
 Db 469 KAE 471

RESULT 10

CPN\_DROME

ID CPN\_DROME STANDARD; PRT; 865 AA.  
 AC Q02910;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Calphotin.  
 GN CPN OR CAP.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=93165729; PubMed=8094559;  
 RA Martin J.H., Benzer S., Rudnicka M., Miller C.A.;  
 RT "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=93165730; PubMed=8434015;  
 RA Ballinger D.G., Xue N., Harshman K.D.;  
 RT "A Drosophila photoreceptor cell-specific protein, calphotin, binds  
 RT calcium and contains a leucine zipper.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).  
 CC -!- FUNCTION: Might function as a calcium-sequestering "sponge" to  
 CC regulate the amount of free cytoplasmic calcium. It binds 0.3 mole  
 CC of Ca(2+) per mole of protein.  
 CC -!- SUBUNIT: Homodimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.  
 CC -!- TISSUE SPECIFICITY: Soma and axons of photoreceptor cells of  
 CC compound eyes and ocelli.  
 CC -!- DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell  
 CC development.  
 CC -----  
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 CC -----

DR EMBL; L02111; AAA28405.1; -.  
 DR EMBL; L05080; AAA28420.1; -.  
 DR PIR; A47282; A47282.  
 DR PIR; A47283; A47283.  
 DR FlyBase; FBgn0010218; Cpn.  
 DR GO; GO:0005509; F:calcium ion binding; IDA.  
 KW Calcium-binding.  
 FT CONFLICT 36 36 A -> AVAPAVVA (IN REF. 2).  
 FT CONFLICT 43 43 I -> T (IN REF. 2).  
 FT CONFLICT 64 64 I -> V (IN REF. 2).  
 FT CONFLICT 76 76 T -> A (IN REF. 2).  
 FT CONFLICT 100 100 P -> PP (IN REF. 2).  
 FT CONFLICT 126 127 VQ -> AP (IN REF. 2).  
 FT CONFLICT 154 154 I -> V (IN REF. 2).  
 FT CONFLICT 160 160 S -> T (IN REF. 2).  
 FT CONFLICT 534 534 A -> E (IN REF. 2).  
 FT CONFLICT 699 699 I -> T (IN REF. 2).  
 FT CONFLICT 703 703 V -> L (IN REF. 2).  
 FT CONFLICT 721 721 D -> E (IN REF. 2).  
 SQ SEQUENCE 865 AA; 84781 MW; 2110417E0B0E7CFE CRC64;

Query Match 5.5%; Score 324.5; DB 1; Length 865;  
 Best Local Similarity 22.3%; Pred. No. 1.1e-05;  
 Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGLPAAPPVAPERQPSWDPSVVSSTVP 118  
 | : ||| | | ||: | || | : | | | : | : |  
 Db 9 PVSAPVAAPV-TPSAVAAPVQVWSPAAPVAPAAPIAVTPVAPPPTLASVQPATV--TIP 65  
  
 Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPPAP----APAAPP--ST 172  
 ||:|:|:|:|:| || | |||: || : || | || || : |  
 Db 66 APAPIAAASVTP---VASVAPPVVAAPTTPAA--SPVSTPVAVAQIPVAVSAPVAPPVVAAT 121  
  
 Qy 173 PAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF 232  
 | : : |: | || |: || | :|:|: |:  
 Db 122 PTPVVQIPVAAPVIAT-----PPVAASA-----PT----PAAVTPVISPVIAS-- 160  
  
 Qy 233 KEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSV 292  
 |:| | | |: : | :: | : |  
 Db 161 -----PPVVPANTT---VPVAAPVAAPVAAVPVAPVLAP-----AV 194  
  
 Qy 293 SPKAESAVIVAN-----PREEIIIVKNKDEEEKLVSNILHXQQLPTALTCLKVKEDEVVS 347  
 :| | :|| | || | :| : |:| ||:  
 Db 195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVVA 234  
  
 Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407  
 : | : | | | | | : : :|: : : |  
 Db 235 T---KPLAAAEPVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280  
  
 Qy 408 KKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467  
 || : : |:| || ||  
 Db 281 -----ASTEPPV---AAATLTTPAPETPAL----- 301  
  
 Qy 468 LLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527  
 | :| | || | |  
 Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579  
 | | : | : | : | | : | | : | | : | | : | |  
 Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371

Qy 580 -AQLCPSEFESEATPSPVLDPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHE 638  
 | | : : | : | | : : | : | | : | | : | | :  
 Db 372 PATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVVAEET 431

Qy 639 PENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEP 697  
 | | | | : : : | : : | | : | | : | | : : | |  
 Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSADAPAEAPSAAPIVSTPPTTASVPETTAPPA 491

Qy 698 P-----DFSDYSEMAKVEQVPDPHSEL-----VEDSSPDSEPVDLFSDD SIP--DVPQK 744  
 | | | | : | | | : | | : | | : | | : | : |  
 Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIIEPVEPPAPIPDL 550

Qy 745 QDETVM LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEV 804  
 : : | : | : : | : : : : | : : : : |  
 Db 551 LEQTTSVP AVEAAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603

Qy 805 STLSKKKEKIPLQ---MEELSTAVYSNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLI 860  
 | : | | : : : : | | : | | | | | | | :  
 Db 604 SLATPTEPIPV EAPVVIQEAVDAV-----EVPVTETST---SIP-ETTVEFPEAV 649

Qy 861 SSKTDSF SKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDL SL 906  
 : | : | : | : : : : | | | | | : : :  
 Db 650 AEKV-----LDPAITEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701

Qy 907 KNIQPKVEEKISFSDDFSKNGSATS KVL L---LP-----PDVSALG----- 944  
 | | | : : : : : : : : : : | | : | |  
 Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760

Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLY 996  
 : | | : | | : | | : | : : | | | : | : | |  
 Db 761 ITAGDNP DNTSVGISEVV-PTIAEKPV EEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814

Qy 997 WRDIKKTGV 1005  
 | | : : | |  
 Db 815 -RDLQTTDV 822

RESULT 11

PCLO\_HUMAN

ID PCLO\_HUMAN STANDARD; PRT; 5147 AA.  
 AC Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Piccolo protein (Aczonin) (Fragments).  
 GN PCLO OR ACZ OR KIAA0559.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-759 FROM N.A.  
 RC TISSUE=Brain;

RX MEDLINE=99439764; PubMed=10508862;  
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,  
 RA Kilimann M.W.;  
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active  
 RT zones, shares homology regions with rim and bassoon and binds  
 RT profilin.";  
 RL J. Cell Biol. 147:151-162(1999).  
 RN [2]  
 RP SEQUENCE OF 552-4404 FROM N.A.  
 RA Kraemer J., Wollam C., Wohldmann P., McGrane B.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 RN [4]  
 RP SEQUENCE OF 4405-4439 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 4405-5147 FROM N.A.  
 RA Kalicki J., Elliott G.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: May act as a scaffolding protein involved in the  
 CC organization of synaptic active zones and in synaptic vesicle  
 CC trafficking (By similarity).  
 CC -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of  
 CC synaptic junctions (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:

```

CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9Y6V0-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925,
CC      VSP_003926, VSP_003927;
CC      Note=No experimental confirmation available;
CC      -!- DOMAIN: C2 domain 1 is involved in binding calcium and
CC      phospholipids. Calcium binds with low affinity but with high
CC      specificity and induces a large conformational change.
CC      -!- SIMILARITY: Contains 2 C2 domains.
CC      -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y19188; CAB60727.1; -.
DR      EMBL; AC004903; AAD20936.1; -.
DR      EMBL; AC004886; AAD21789.1; -.
DR      EMBL; AB011131; BAA25485.1; -.
DR      EMBL; BC001304; AAH01304.1; -.
DR      EMBL; AC004082; AAB97937.1; -.
DR      PIR; T00634; T00634.
DR      HSSP; P04410; 1A25.
DR      Genew; HGNC:13406; PCLO.
DR      MIM; 604918; -.
DR      GO; GO:0005856; C:cytoskeleton; NAS.
DR      GO; GO:0045202; C:synaptic junction; ISS.
DR      GO; GO:0005509; F:calcium ion binding; ISS.
DR      GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
DR      GO; GO:0005522; F:profilin binding; ISS.
DR      GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR      GO; GO:0016080; P:synaptic vesicle targeting; ISS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001565; Synaptotagmin.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
KW      Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW      Repeat; Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      400      465      10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT                                     P-A-K-P-Q-P-Q-Q-P-X.
FT      ZN_FING      499      523      C4-TYPE (POTENTIAL).
FT      ZN_FING      969      992      C4-TYPE (POTENTIAL).
FT      NON_CONS     1010     1011
FT      DOMAIN      2300     2325      POLY-PRO.
FT      DOMAIN      4391     4442      PDZ.
FT      DOMAIN      4544     4633      C2 DOMAIN 1.

```

FT	DOMAIN	5031	5121	C2 DOMAIN 2.
FT	VARSPLIC	4404	4404	S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
FT				QTGKLMEG (in isoform 2).
FT				/FTId=VSP_003923.
FT	VARSPLIC	4534	4534	K -> KPTDGTKVVSHPITGEIQ (in isoform 2).
FT				/FTId=VSP_003924.
FT	VARSPLIC	4576	4576	G -> GQVMVQNAS (in isoform 2).
FT				/FTId=VSP_003925.
FT	VARSPLIC	4757	4761	TAHKS -> SKRRK (in isoform 2).
FT				/FTId=VSP_003926.
FT	VARSPLIC	4762	5147	Missing (in isoform 2).
FT				/FTId=VSP_003927.
SQ	SEQUENCE	5147 AA;	563537 MW;	CD5D84990498CD3C CRC64;

Query Match 5.4%; Score 320; DB 1; Length 5147;  
 Best Local Similarity 21.8%; Pred. No. 0.00015;  
 Matches 260; Conservative 152; Mismatches 440; Indels 340; Gaps 61;

Qy	8	PLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAP	67
		:         :    :	
Db	260	PSLPSPSKPPIQQPTPGKPPAQQPGHEKSQPG-----PAKPPAQPSGLT	303
Qy	68	VPTAPAAGA---PLMDFGNDFVPPAPRGPLPAAPPV-----	100
		:	
Db	304	KPLAQQPGTVKPPVQPPGTTKPPAQPLG--PAKPPAQQTGSEKPSSEQPGPKALAQPPGV	361
Qy	101	--APERQPSWDPSPVSVSTVPAPSPLS-----AAVSPSKLPEDDEPPA-----RPP	144
		:      :       :     :    :   : :	
Db	362	GKTPAQQPG-PAKPPTQQVGTGPKPLAQQPLQSPAKAPGPTKTPAQTKPPSQQPGSTKPP	420
Qy	145	P--PPPASVSPQAEPVWTPPAPAP-AAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGN	201
		:   :     :	
Db	421	PQQPGPAKPSPPQPGSTKPPSQPGSAKPSA-----QQPSP	456
Qy	202	TISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKE	261
		:   :   : :     :     :     :	
Db	457	AKPSAQQ-FTKPVSTGFGKPLQPPTVSPSAKQPPSQGLPKTICPL----CNTTELLH	510
Qy	262	VSEKA-----KTLII-----DRDLTEFSE-----LEYSEMGSFSVSPKA----	296
		:   :        :   :	
Db	511	VPEKANFNTCTECQTTVCSLCGFNPNPHLTEAKEWLCCLNCQMKRALGGDLAPVPSSQPK	570
Qy	297	-----ESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQEL-----PTALTCLVKED	343
		: : :         :        :	
Db	571	LKTAPVTTTSAVSKSSPQPQQTSPKKDAAPK-----QDLSKAPEPKPPPLVKQP	620
Qy	344	EVSSEKAK-----DSFNEKRVAVEAPMREE-----YADFKPFERVWEVKDSKEDSDM	391
		:         : :   :        :     :  :	
Db	621	TLHGSPSAKAKQPPEADSLSKPAPPKEPSVPSEQDKAPVADDKP----KQPKMVKPTTDL	676
Qy	392	LAAGGKIESNLESKVD---KKCFADSLEQTNHEKDSESSNDDTSFSTPEGIKDRSGAYI	448
		:: :   :     : :   : : :        :	
Db	677	VSS-----SSATTKPDIPSSKVSQAEEKTTPPLKTDPAKPSQSFPPTGEKV-----	723
Qy	449	TCAPFN-----PAATESIATNIFPLLE-----DPTSENXTDEKKIEEKKAIQIVTEKN	495
		:    :   :       :	
Db	724	--TPFDSKAIPRPASDSKIISHPGPSSESKGQKQVDPV-----QKKEEPKKAQTKMSPK	775

Qy 496 TSTK-----TSNPFFVAAQDSETDYVTTD-----NLTKVTEEVVANMPEGLT 537  
 | | | | : || :| : | : |  
 Db 776 PDAKPMPKGSPTPPGPRPTAGQTVPTPQQSPKPKQEQSRRFSLNLGSITD---APKSQPTT 832  
 Qy 538 PDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA--AQLCPSEFESEATPSP 595  
 | || ||| : : | | : : | : | : | : | : |  
 Db 833 P---QET-----VTGKLFGFGASI-FSQASNLISTAGQPGPHSQSGPGAPMKQA-PAP 880  
 Qy 596 VLPDIVMEAPLNSA-VPSAGASVI-----QPSSSPLEASSVNYESIK--HEPENPPPY 645  
 | : : | | | | : : || : : | : |||  
 Db 881 SQPPTSQGPSTGQAPPAPAKSIPVKKETKAPAAEKLEPKAEQAPTVMKRTETETKPPPI 940  
 Qy 646 EEAMSVSLKVSIGIKEEIKEPENINAALQETEAPYISIACDLIK-ETKLSAEPAPDFSDYS 704  
 : : | : : || : : : | | | : : | : : :  
 Db 941 KDSKSLT-----AEPQKAVLPTKLEKSPKPESTCPLCKTELNIGSKDPNFTCT 990  
 Qy 705 EMAKVE-----QVPDHSSELVE-----DSSPDSEPVDLFSDDS--- 737  
 | | : | : | : | : : : |  
 Db 991 ECKNQVCNLCGFNPTPHLTENCQTQRAISGQLGDIRKMPPAPSGPKASMPVPTESSSQK 1050  
 Qy 738 --IPDVPQ-----KQD-----ETVML--VKESLTETSFESMIEYENKEKLSALPPEGG 781  
 : | || || : | : | || : | : | : | : |  
 Db 1051 TAVP--PQVKLVKKQEVEKTEAEKVILEKVKETLSMEKIPPMVTTDQKQESKLEKDKA 1108  
 Qy 782 KPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRET 841  
 | | | | : : | : : | : | : | : | : |  
 Db 1109 SALQE--KKPLPEEK-KLIPEE-EKIRSEEKKPLLEKKPTP----EDKLLPEAKTSAP 1160  
 Qy 842 ETFSD---SSPIEIDE-FPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA-GSLP 896  
 | : : | : | : : || | : : : | | |||  
 Db 1161 EEQKHDLKSKVQVIAEEKLEGRVAPKTVQEGK-----QPQTKMEGLPSGTPQSLP 1210  
 Qy 897 CTCLPHDLSLKNI-----QPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQ----- 947  
 : | : | | || | : | : : | : | : | :  
 Db 1211 KED---DKTTKTIKEQPQPCTAKPDQEKEDDKSDTSSSQPKSPQGLSDTGYSSDGISS 1267  
 Qy 948 --AEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGK--TSVVDLL 995  
 || | : : || : | | | : : || : | : | : |  
 Db 1268 SLGEIPSLIPTD--EKDILKGLKKDSFSQESSPSS--PSDLAKLESTVLSIL 1315

# RESULT 12

## PCLO\_MOUSE

ID PCLO\_MOUSE STANDARD; PRT; 5038 AA.  
 AC Q9QYX7; Q9QYX6; Q9QZJ0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Piccolo protein (Presynaptic cytomatrix protein) (Aczonin) (Brain-  
 DE derived HLMN protein).  
 GN PCLO OR ACZ.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, ALTERNATIVE SPLICING,  
 RP TISSUE SPECIFICITY, AND INTERACTION WITH PROFILIN.  
 RC TISSUE=Brain;  
 RX MEDLINE=99439764; PubMed=10508862;  
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,  
 RA Kilimann M.W.;  
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active  
 RT zones, shares homology regions with rim and bassoon and binds  
 RT profilin.";  
 RL J. Cell Biol. 147:151-162(1999).  
 RN [2]  
 RP REVISIONS.  
 RA Kilimann M.W.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 4502-4682 FROM N.A.  
 RC TISSUE=Brain;  
 RA Huang W., Jin W., Huang C., Chen B., Zhang J., Ju G.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP INTERACTION WITH RIMS2.  
 RX MEDLINE=22384373; PubMed=12401793;  
 RA Fujimoto K., Shibasaki T., Yokoi N., Kashima Y., Matsumoto M.,  
 RA Sasaki T., Tajima N., Iwanaga T., Seino S.;  
 RT "Piccolo, a Ca2+ sensor in pancreatic beta-cells. Involvement of  
 RT cAMP-GEFII.Rim2.Piccolo complex in cAMP-dependent exocytosis.";  
 RL J. Biol. Chem. 277:50497-50502(2002).  
 CC -!- FUNCTION: May act as a scaffolding protein involved in the  
 CC organization of synaptic active zones and in synaptic vesicle  
 CC trafficking.  
 CC -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin.  
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of  
 CC synaptic junctions.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9QYX7-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9QYX7-2; Sequence=VSP\_003928, VSP\_003929;  
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Low levels found in  
 CC stomach. Not detected in other tissues analyzed including adrenal  
 CC gland, testis and pancreas.  
 CC -!- DOMAIN: C2 domain 1 is involved in binding calcium and  
 CC phospholipids. Calcium binds with low affinity but with high  
 CC specificity and induces a large conformational change.  
 CC -!- SIMILARITY: Contains 2 C2 domains.  
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Y19185; CAB60731.2; -.



DR EMBL; Y19186; CAB60732.2; -.  
 DR EMBL; AF181269; AAD55786.2; -.  
 DR HSSP; P04410; 1A25.  
 DR MGD; MGI:1349390; Pclo.  
 DR GO; GO:0045202; C:synaptic junction; IDA.  
 DR GO; GO:0005509; F:calcium ion binding; ISS.  
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.  
 DR GO; GO:0005522; F:profilin binding; IDA.  
 DR GO; GO:0019933; P:cAMP-mediated signaling; IDA.  
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.  
 DR GO; GO:0030073; P:insulin secretion; IDA.  
 DR GO; GO:0017157; P:regulation of exocytosis; IDA.  
 DR GO; GO:0016080; P:synaptic vesicle targeting; NAS.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR008899; Znf\_piccolo.  
 DR Pfam; PF00168; C2; 2.  
 DR Pfam; PF00595; PDZ; 1.  
 DR Pfam; PF05715; Zf\_piccolo; 2.  
 DR SMART; SM00239; C2; 2.  
 DR SMART; SM00228; PDZ; 1.  
 DR PROSITE; PS00499; C2\_DOMAIN\_1; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN\_2; 2.  
 DR PROSITE; PS50106; PDZ; 1.  
 KW Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;  
 KW Repeat; Alternative splicing.  
 FT DOMAIN 371 470 10 X 10 AA TANDEM APPROXIMATE REPEATS OF  
 FT P-A-K-P-Q-P-Q-Q-P-X.  
 FT ZN\_FING 502 526 C4-TYPE (POTENTIAL).  
 FT ZN\_FING 967 990 C4-TYPE (POTENTIAL).  
 FT DOMAIN 2305 2329 POLY-PRO.  
 FT DOMAIN 4394 4488 PDZ.  
 FT DOMAIN 4607 4705 C2 DOMAIN 1.  
 FT DOMAIN 4922 5012 C2 DOMAIN 2.  
 FT VARSPLIC 4829 4833 TKPTN -> SKRRK (in isoform 2).  
 FT /FTId=VSP\_003928.  
 FT VARSPLIC 4834 5038 Missing (in isoform 2).  
 FT /FTId=VSP\_003929.  
 SQ SEQUENCE 5038 AA; 547600 MW; DADA460CF3B40888 CRC64;

Query Match 5.3%; Score 315; DB 1; Length 5038;  
 Best Local Similarity 22.0%; Pred. No. 0.00023;  
 Matches 254; Conservative 136; Mismatches 435; Indels 328; Gaps 57;

Qy 57 RKPA--AGLSAAPVPTAPAAGAPLMDFG---NDFVPPAPR-----GPLPAAPPVAPE 103  
 : || || :| | | | | : | :| | :|  
 Db 288 KSPAQPAGTGKSPAQPPVTAKPPAQQAGLEKTSLQQPGPKSLAQTPGQGVPPGPAKSPA 347  
 Qy 104 RQ-----PSWDPSP-VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ-A 155  
 :| | :| | :| | | :| | | | :| | | ||  
 Db 348 QQPGTAKLPAQQPGPQTASKVPGPTKTPAQLSGPGKTPAQQPGPTKPSPPQPIPAKPQPQ 407  
 Qy 156 EPVWT---PPAPAPAAPP---STPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED 209  
 :|| | | ||| | ||| : : : | | | | :  
 Db 408 QPVATKPPQPPAPAKPQPQHPTPAKPQPQOPTPA-----KPQPQOPTPAKPQP 456  
 Qy 210 FPSVLLETAASXPSLS-----PLSA--ASFKEHEYLGNLSTVLP---TEGTLQENV 256

Db	457	QHPGLGKPSAQQPSKISQTVTGRPLQAPPTSAAQAPAQGLSKTICPLCNTTELLHTPE	516
Qy	257	EASKEVSEKAKTLLI-----DRDLTEFSEL-----EYSEMGSSFSVSPKA	296
Db	517	KANFNTCTECQSTVCSLCGFNPNPHLTEIKEWLCLNCQMQRALGGELAAIPSSPQPTPKA	576
Qy	297	ESAVIV-----ANPREELIVKN---KDEEEK----LVSNNILHX-----QQE	331
Db	577	ASVQPATASKSPVPSQQASPKKELPSKQDSPKAPESKKPPPLVKQPTLHGPTPATAPQPP	636
Qy	332	LPTALTCLV--KEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS	389
Db	637	VAEALPKPAPPKKPSAALPEQAK-----APV----ADVEPKQP--KTETLTDS	679
Qy	390	DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYIT	449
Db	680	PSSAAATSKPAILSSQVQ----AQAVTTAPPLKTDSAKTSQSFPPTGD-----T	725
Qy	450	CAPFN-----PAATESIATNIFLLEDPTSENXTD-EKKIEEKKAQIVTEKNTSTKTSN	502
Db	726	ITPLDSKAMPRPASDSKIVSH-----PGPTSESKDPVQKKEPKKAQTKVTPKPDTK---	777
Qy	503	PFFVAAQDSETDYVTTDNLTKEEV-----VANMPEGLTPDLVQEACE	546
Db	778	PVPKGSPTPSGTRPTTGQATPQSQQPPKPPEQSRRFSNLGGIADAPKS-QPTTPQET--	834
Qy	547	SELNEVTGTKIAYETKMDLVQTESEVMQESLYPAAQLCPSFESEATPSPVLP----DIVM	602
Db	835	-----VTGKLFGFGASI-FSQASNLIS----TAGQQAPHPQTGPAAPSKQAPPPSQTLAA	884
Qy	603	EAPLNSA--VPSAGASVIQ-----PSSSPLEASSVNYESI-----KHEP---ENPP	643
Db	885	QGPPKSTGQHPSAPAKTTAVKKETKGPAAENLEAKPAQAPTVMKAEKDKKHPPGKVSPPP	944
Qy	644	PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISACDLIK-ETKLSAEPAPDFSD	702
Db	945	P-----TEPEKAVLAQKPDKTTKPKPACPLCRTELNVGSQDPPNFNT	986
Qy	703	YSEMAKVE-----QVPVDHSELVE-----DSSPDSEPVD	731
Db	987	CTECKNQVCNLCGFNPTPHLTEIQEWLCLNCQTQRAISGQLGDMDKMPPASSGPKASPVP	1046
Qy	732	LFSD-----DSIPDVPQKQDETV-----MLVKESLT	757
Db	1047	APAEPPPQKTPTAAHAKGKKKETEVKAETEKQIPEKETPSIEKTPPAVATDQKLESEVT	1106
Qy	758	ETSFESMIEYENKEKLSAL-----PPEGKPYLESFKLSLDNTKDTLLPDEVSTLSK	809
Db	1107	KSLVSVLPKPKPSEEEKALPADKKEKKPPAAEAPPLEKKPIPDQK--LPPDAKPSASE	1164
Qy	810	KEKIPLQMEELSTAVYSNDDLFIKSEAQIR-ETETFSDSPIEIIDFPTLISSKTDSFS	868
Db	1165	GEE---KRDLLKAHVQIPEEGPIKVASLACEGEQQPDTRPEDLPGATPQTLPKD-----	1216
Qy	869	KLAREYTDLEVSHKSEIANAPDGAG--SLPCTELPHDLS--LKNIQPKVEEKISFSDDFS	924

Db 1217 ---RQKESRDVTQPQAEGTAKEGRGEPKDRTEKEEDKSDTSSSSQQPKSPQGLS-DTGYS 1272  
 QY 925 KNGSATSKVLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSA 984  
 :| : | || || |:: ||: | | |: :: |||: :  
 Db 1273 SDGISGS-----LG----EIPSLIPSD--EKDLLKGLKKDSFSQESSPSS--PS 1313  
 QY 985 DLGK--TSVVDLL 995  
 || | :|: :|  
 Db 1314 DLAKLESTVLSIL 1326

RESULT 13

ANK2\_HUMAN

ID ANK2\_HUMAN STANDARD; PRT; 3924 AA.  
 AC Q01484; Q01485;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).  
 GN ANK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC TISSUE=Brain stem;  
 RX MEDLINE=91302466; PubMed=1830053;  
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;  
 RT "Isolation and characterization of cDNAs encoding human brain  
 RT ankyrins reveal a family of alternatively spliced genes.";  
 RL J. Cell Biol. 114:241-253(1991).  
 RN [2]  
 RP REVISIONS.  
 RA Carpenter S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain stem;  
 RX MEDLINE=94075409; PubMed=8253844;  
 RA Chan W., Kordeli E., Bennett V.;  
 RT "440-kD ankyrinB: structure of the major developmentally regulated  
 RT domain and selective localization in unmyelinated axons.";  
 RL J. Cell Biol. 123:1463-1473(1993).  
 RN [4]  
 RP SEQUENCE OF 463-495 FROM N.A.  
 RX MEDLINE=92009921; PubMed=1833308;  
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,  
 RA Lux S.E., Ward D.C., Forget B.G.;  
 RT "Isolation and chromosomal localization of a novel nonerythroid  
 RT ankyrin gene.";  
 RL Genomics 10:858-866(1991).  
 CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal  
 CC elements. Also bind to cytoskeletal proteins.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;

```

CC      IsoId=Q01484-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
CC      Name=3;
CC      IsoId=Q01484-3; Sequence=VSP_000268;
CC      -!- TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial
CC          cells throughout the brain.
CC      -!- PTM: Phosphorylated at multiple sites by different protein kinases
CC          and each phosphorylation event regulates the protein's structure
CC          and function (Potential).
CC      -!- SIMILARITY: Contains 23 ANK repeats.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56957; CAA40278.1; -.
DR      EMBL; X56958; CAA40279.2; -.
DR      EMBL; Z26634; CAB42644.1; -.
DR      EMBL; M37123; AAA62828.1; -.
DR      PIR; S37431; S37431.
DR      HSSP; P42771; 1DC2.
DR      Genew; HGNC:493; ANK2.
DR      MIM; 106410; -.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00023; ank; 24.
DR      Pfam; PF00531; death; 1.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      SMART; SM00248; ANK; 22.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50088; ANK_REPEAT; 20.
DR      PROSITE; PS50297; ANK_REP_REGION; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
KW      Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW      Phosphorylation.
FT      REPEAT      63      92      ANK 1.
FT      REPEAT      96     125     ANK 2.
FT      REPEAT     129     158     ANK 3.
FT      REPEAT     162     191     ANK 4.
FT      REPEAT     193     220     ANK 5.
FT      REPEAT     232     261     ANK 6.
FT      REPEAT     265     294     ANK 7.
FT      REPEAT     298     327     ANK 8.
FT      REPEAT     331     360     ANK 9.
FT      REPEAT     364     393     ANK 10.
FT      REPEAT     397     426     ANK 11.
FT      REPEAT     430     459     ANK 12.
FT      REPEAT     463     492     ANK 13.

```

FT	REPEAT	496	525	ANK 14.
FT	REPEAT	529	558	ANK 15.
FT	REPEAT	562	591	ANK 16.
FT	REPEAT	595	624	ANK 17.
FT	REPEAT	628	657	ANK 18.
FT	REPEAT	661	690	ANK 19.
FT	REPEAT	694	723	ANK 20.
FT	REPEAT	727	756	ANK 21.
FT	REPEAT	760	789	ANK 22.
FT	REPEAT	793	822	ANK 23.
FT	DOMAIN	1773	1950	REPEAT-RICH REGION.
FT	REPEAT	1773	1784	REPEAT A.
FT	REPEAT	1785	1796	REPEAT A.
FT	REPEAT	1797	1808	REPEAT A.
FT	REPEAT	1809	1820	REPEAT A.
FT	REPEAT	1821	1832	REPEAT A.
FT	REPEAT	1833	1844	REPEAT A.
FT	REPEAT	1845	1856	REPEAT A.
FT	REPEAT	1857	1867	REPEAT A (APPROXIMATE).
FT	REPEAT	1868	1879	REPEAT A.
FT	REPEAT	1880	1891	REPEAT A.
FT	REPEAT	1892	1902	REPEAT A (APPROXIMATE).
FT	REPEAT	1903	1914	REPEAT A.
FT	REPEAT	1915	1926	REPEAT A.
FT	REPEAT	1927	1938	REPEAT A.
FT	REPEAT	1939	1950	REPEAT A.
FT	DOMAIN	3536	3620	DEATH.
FT	VARSPPLIC	1039	1039	Q -> QFLGKLHLPTAPPPLNEGESLVSRIQLGPPGK
FT				(in isoform 2).
FT				/FTId=VSP_000267.
FT	VARSPPLIC	1444	3528	Missing (in isoform 2 and isoform 3).
FT				/FTId=VSP_000268.
FT	CONFLICT	475	476	GQ -> PE (IN REF. 4).
FT	CONFLICT	971	971	I -> S (IN REF. 1).
FT	CONFLICT	3581	3582	QY -> HA (IN REF. 1).
FT	CONFLICT	3586	3586	I -> Y (IN REF. 1).
SQ	SEQUENCE	3924	AA; 430337 MW; 52AC496C428E29D2 CRC64;	

Query Match 5.0%; Score 299; DB 1; Length 3924;  
 Best Local Similarity 21.5%; Pred. No. 0.00069;  
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

QY	14	DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK	58
		:      : :::::    :	
Db	1648	DIPDETQSTQKQHKPSLGIKKPVRRKLKEKQKQKEEGLQASAEKAEKKGSSEESLGED	1707
QY	59	PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----	92
		:  :      :  ::   :  :	
Db	1708	P--GLAPEPLPTVKAT-SPLIEETPIGSIKDKVKALQKRVEDEQKGRSKLPPIRVKGKEDV	1764
QY	93	-----PLPAA-PPVAPERQPSWDPS-----VSSTVPAPSPL	123
		:	
Db	1765	PKKTTHRPHPAASPSLKSERHAFGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV	1824
QY	124	SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW	159
		:          :       : : :	
Db	1825	SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSKTERHPPVSPSGKTDKRPPV-	1883

Qy	160	TPPAPAPAAPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLL	216
Db	1884	SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLPVSPSG	1934
Qy	217	TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT	268
Db	1935	KTEKQPPVSPTS KTERIEETMSVRELMAKAFQSGQDPSKHKTGLFEHKSQKQKQPEKGKV	1994
Qy	269	-----LLIDRDLTEFSELEYSEMSSFSVSPKAES--AVIVANPREEIIIVKNKDE--	316
Db	1995	RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAESKRGVRVSS----IGVKKEDAAG	2049
Qy	317	-EEKLVSNNI-----LHXQQELPTALTCLVKE-----DEVV	346
Db	2050	GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGDMDLQISPDRTSTDFSEVI	2107
Qy	347	SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED-----	388
Db	2108	KQLEDNDKYQQFRLSEETEKALHLQVLTSPFNTTFFLDYMKDEFLPALSLQSGALDG	2167
Qy	389	-SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDSESSNDDTSFPSTPEGIKDRS	444
Db	2168	SSESLKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT	2225
Qy	445	GAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPF	504
Db	2226	G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTEDSETSTESFQKE	2277
Qy	505	FVAAQDSETDYVTTDNLTKVTEEVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKM	563
Db	2278	ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT---EAAACDEGQRTFGSS-AHKT--	2330
Qy	564	DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVL-----PDIVMEAP--LNSAV	610
Db	2331	---QTDSEAQES-----TATSDETKALPLPEASVKTDGTESKPGQGVIRSPQGLELAL	2380
Qy	611	PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVS	657
Db	2381	PSRDSEVL SAVADDSLAVSHKDSLEASPVLEDNSSHKTPDSLEPSPLKESPCRDSLESSP	2440
Qy	658	IKEEIKE---PEN--INAALQETE--APYISIACDLIKETKLSAEPAPDFSDYSEMAKVE	710
Db	2441	VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE	2490
Qy	711	QVPDPHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETS FEMI	765
Db	2491	Q-----TSLMESSGKSPLSPDTPSSEEVSYEVTPKTTDVSTPKPAVIHECAEED-----	2539
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK---EKIPLQMEELS	821
Db	2540	DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAKQKRDKKEPKQEES	2589
Qy	822	TAVYSNDDLFISKEA-QIRETETFSDDSPIEIIDFPTLISSKTD SFSKLAREYTDLEVS	880
Db	2590	S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSES RKVSSSSS-----	2633

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QY      881 HKSEIANAPDGAGS-----LPCTELPHDLSLKN-----IQPKVEEKISF--SDD 922
      : |:|   || |   | : || :   :   || | :: :| ::|
Db      2634 -EPELAQLKKGADSGLLPEPVIRVQPPSPLPSSMDSNSSPEEVQFQPVVSKQYTFKMED 2692

QY      923 FSKNGSATSKVLLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPSP-----TEKEDRS 977
      :   : :   ||::| | |   || |||
Db      2693 TQEEPGKSEE-----EKDSESHLAEDRHAVSTEAEDRS 2725

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# RESULT 14

## MAPB\_HUMAN

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ID      MAPB_HUMAN      STANDARD;      PRT; 2468 AA.
AC      P46821;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
DE      LC1].
GN      MAP1B.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Fetal brain;
RX      MEDLINE=95104835; PubMed=7806212;
RA      Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
RT      "Cloning of human microtubule-associated protein 1B and the
RT      identification of a related gene on chromosome 15.";
RL      Genomics 22:273-280(1994).
CC      -!- FUNCTION: The function of brain MAPS is essentially unknown.
CC      Phosphorylated MAP1B may play a role in the cytoskeletal changes
CC      that accompany neurite extension. Possibly MAP1B Binds to at least
CC      two tubulin subunits in the polymer, and this bridging of subunits
CC      might be involved in nucleating microtubule polymerization and in
CC      stabilizing microtubules.
CC      -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
CC      with MAP1A and MAP1B proteins.
CC      -!- DOMAIN: Has a highly basic region with many copies of the sequence
CC      KKEE and KKEI/V, repeated but not at fixed intervals, which is
CC      responsible for the binding of MAP1B to microtubules.
CC      -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
CC      from MAP1B by proteolytic processing. It is free to associate with
CC      both MAP1A and MAP1B. It interacts with the amino-terminal region
CC      of MAP1B (By similarity).
CC      -!- SIMILARITY: TO MAP1A.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L06237; AAA18904.1; -.

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DR Genew; HGNC:6836; MAP1B.  
 DR MIM; 157129; -.  
 DR GO; GO:0005875; C:microtubule associated complex; TAS.  
 DR InterPro; IPR000102; MAP1B\_neuraxin.  
 DR Pfam; PF00414; MAP1B\_neuraxin; 10.  
 DR PROSITE; PS00230; MAP1B\_NEURAXIN; 6.  
 KW Microtubule; Repeat; Phosphorylation.  
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.  
 FT REPEAT 1878 1894 MAP1B 1.  
 FT REPEAT 1895 1911 MAP1B 2.  
 FT REPEAT 1912 1928 MAP1B 3.  
 FT REPEAT 1929 1945 MAP1B 4.  
 FT REPEAT 1946 1962 MAP1B 5.  
 FT REPEAT 1963 1979 MAP1B 6.  
 FT REPEAT 1997 2013 MAP1B 7.  
 FT REPEAT 2014 2030 MAP1B 8.  
 FT REPEAT 2031 2047 MAP1B 9.  
 FT REPEAT 2048 2064 MAP1B 10.  
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY  
 FT KKEE AND KKEI/V REPEATS).  
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 5.0%; Score 296.5; DB 1; Length 2468;  
 Best Local Similarity 21.5%; Pred. No. 0.00049;  
 Matches 264; Conservative 148; Mismatches 459; Indels 355; Gaps 59;

Qy 2 EDLDQSPLVSSS-DSPRPQPAFKYQ---FVREP-----EDEE 35  
 || :: ||:| || : : | : :|| | :  
 Db 956 EDGEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGEAEQ 1015  
  
 Qy 36 EEEEEEEDEDEDLEELEEV-LERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPL 94  
 ||| :|||: || | | |: | | | | | :| | |  
 Db 1016 SEEEADEEDKAEDAREEEYEPEKMEAEDYVMAVVDKAAEAGGAEQYGFLLTPTKQLG-- 1073  
  
 Qy 95 PAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ 154  
 :| |:|: | |:| | | | |:| | | :  
 Db 1074 ----AQSPGREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTATSGYT 1120  
  
 Qy 155 AEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----D 209  
 : | | | | | :| : | | |  
 Db 1121 QSTIEISSEPTPMDEMSTP-----RDVMSDETNNETESPSQEFVNITK 1164  
  
 Qy 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259  
 : | | | |: :||: | | :| : ||: | : : | : :  
 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFSRSA 1222  
  
 Qy 260 -----KEVSEKAKTLLIDRDLTEF-----SELEYSEMGS---SFS 291  
 || || | | :| | | : :| :||  
 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPSKSPSLSPSPSPLEKTPLGERSVNFS 1280  
  
 Qy 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328  
 :| | |: | :| :|: : : |:| | : : |  
 Db 1281 LTPNEIKVSAEAEVAPVSPEVTQEVVEEHCASPEDKTLEVVSQSQSVTGSAGHTPYQSP 1340  
  
 Qy 329 ----QQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383  
 ||| : : | | : |:| | :|| | : | | :|  
 Db 1341 TDEKSSHLPTEV--IEKPPAVPVSFESDAKDENERASVSPMDEPVPDSESPIEKVLSPL 1398



Qy 384 DSKEDSDMLAAGGKIESNLESKVDKKCFADSLQTNHEKDSSESNDDTSFPSTPEGIKDR 443  
 | : : | | : | | | : : | | :  
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEKSGKQGSPPQVSPVSE----- 1447

Qy 444 SGAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKK-----IEKK-----A 488  
 : | : : | : | | | : : : : :  
 Db 1448 ----MTSTSLYQDKQEGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSP 1503

Qy 489 QI-----VTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVA--N 531  
 || : : | | : | | : : | : || :  
 Db 1504 QIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDTYSHMEGVASVSTASVATSS 1561

Qy 532 MPEGLTPDLVQEACESELNEVTGKTIAYETKMDLVQTSEVMQES-LYPAAQLCP----- 584  
 || | | : : : | : : : || | : : | : ||  
 Db 1562 FPEPTTDD-VSPSLHAEVGSPPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMSIS 1620

Qy 585 -----SFESEATPSPVLP-DIVMEAPLNSAVPSAGASVI 618  
 | | : : | | | : : | : || | :  
 Db 1621 PPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPDH---PTVGAGVL 1677

Qy 619 Q-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSGIKKEEIKE 664  
 | : | : | : | | | : || : : |  
 Db 1678 HITENGPTVDYSPSDMQDSSLSHKIPMEEPSYTQDNDLSELISVSQVEASPSTSSAHT 1737

Qy 665 PENINAALQETE----AP-----YISIACDLIKE---TKLSAEP-----A 697  
 | | : || | | | : : : || : :  
 Db 1738 PSQIASPLQEDTLSDVAPPRDMSLYASLTSEKVSLEGEKLSPKSDISPLTPRESSPLYS 1797

Qy 698 PDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS----- 734  
 | || : | | : || | : | |  
 Db 1798 PTFSDSTSAVK-EKTATCHS----SSSP---PIDAASAEPYGFRAVLFDTMQHHLALNR 1849

Qy 735 DDSIPDVP-----QKQDET'VMLVKESLTETSFESMIEYENKEKLSALPPE 779  
 | | | : || : || | : | : || : || :  
 Db 1850 DLSTPGLEKDSGGKTPGDFSYAYQKPEET-----TRSPDEEDYDYESYEKTTTRTSDV 1901

Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKAEQIR 839  
 || | | : : : | : | | | | : | | :  
 Db 1902 GGY-YYEKIERTTKSPSDSGYSYE--TIGKTTKTP-----EDGDYSYE--IEKTTTRTP 1950

Qy 840 ETETFSDSSPIEIIIDEFPTLISSKTDs---FSKLAREYTDLEVSHKSEIANAPDGAGSLP 896  
 | : | | | | | : | | : : | | :  
 Db 1951 EEGGYSYD-----ISEKTTSPPEVSGYSYEKTERSRRLLDDISNGYDDS---- 1994

Qy 897 CTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAE-IESIVK 955  
 : | | : : || : : || | : | | :  
 Db 1995 -EDGGHTLGDPSSYSYETTEKITSFPESEGYSETSTKTTTRTPDTSTYCYETAEKITRTPQ 2053

Qy 956 PKVLEKE-----AEKKLPSDTEKE 974  
 | ||| || : :  
 Db 2054 ASTYSYETSDLCYTAEKKSPSEARQD 2079

RESULT 15

MAPB\_RAT

ID MAPB\_RAT

STANDARD;

PRT; 2459 AA.

AC P15205; Q62958; Q9ER21; Q9QW92;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1  
 DE light chain LC1].  
 GN MAP1B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-142 FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
 RX MEDLINE=96257242; PubMed=8666295;  
 RA Liu D., Fischer I.;  
 RT "Isolation and sequencing of the 5' end of the rat microtubule-  
 RT associated protein (MAP1B)-encoding cDNA."  
 RL Gene 172:307-308(1996).  
 RN [2]  
 RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;  
 RX MEDLINE=92347374; PubMed=1639092;  
 RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;  
 RT "Identification of two distinct microtubule binding domains on  
 RT recombinant rat MAP 1B."  
 RL Eur. J. Cell Biol. 57:66-74(1992).  
 RN [3]  
 RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Spinal cord;  
 RX MEDLINE=90059871; PubMed=2555150;  
 RA Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,  
 RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;  
 RT "Neuraxin, a novel putative structural protein of the rat central  
 RT nervous system that is immunologically related to microtubule-  
 RT associated protein 5."  
 RL EMBO J. 8:2879-2888(1989).  
 RN [4]  
 RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.  
 RX MEDLINE=97405699; PubMed=9260743;  
 RA Ma D., Nothias F., Boyne L.J., Fischer I.;  
 RT "Differential regulation of microtubule-associated protein 1B (MAP1B)  
 RT in rat CNS and PNS during development."  
 RL J. Neurosci. Res. 49:319-332(1997).  
 CC -!- FUNCTION: The function of brain MAPS is essentially unknown.  
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes  
 CC that accompany neurite extension. Possibly MAP1B Binds to at least  
 CC two tubulin subunits in the polymer, and this bridging of subunits  
 CC might be involved in nucleating microtubule polymerization and in  
 CC stabilizing microtubules.  
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate  
 CC with MAP1A and MAP1B proteins.  
 CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,  
 CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,  
 CC heart or muscle.  
 CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic  
 CC nerve levels are high early in development but decrease during

CC postnatal development and are low in adults. In dorsal root  
 CC ganglia levels remain high throughout development.  
 CC -!- INDUCTION: By nerve growth factor.  
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence  
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is  
 CC responsible for the binding of MAP1B to microtubules.  
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated  
 CC from MAP1B by proteolytic processing. It is free to associate with  
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region  
 CC of MAP1B (By similarity).  
 CC -!- PTM: Phosphorylated.  
 CC -!- SIMILARITY: TO MAP1A.  
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to  
 CC 2459) was originally described as neuraxin in Ref.3.

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DR EMBL; U52950; AAB17068.1; -.  
 DR EMBL; X60370; CAC16162.1; -.  
 DR EMBL; X16623; CAA34620.1; ALT\_SEQ.  
 DR PIR; A56577; A56577.  
 DR InterPro; IPR000102; MAP1B\_neuraxin.  
 DR Pfam; PF00414; MAP1B\_neuraxin; 10.  
 DR PROSITE; PS00230; MAP1B\_NEURAXIN; 8.  
 KW Microtubule; Repeat; Phosphorylation.

FT	CHAIN	?	2459	MAP1 LIGHT CHAIN LC1.
FT	REPEAT	1869	1885	MAP1B 1.
FT	REPEAT	1886	1902	MAP1B 2.
FT	REPEAT	1903	1919	MAP1B 3.
FT	REPEAT	1920	1936	MAP1B 4.
FT	REPEAT	1937	1953	MAP1B 5.
FT	REPEAT	1954	1970	MAP1B 6.
FT	REPEAT	1988	2004	MAP1B 7.
FT	REPEAT	2005	2021	MAP1B 8.
FT	REPEAT	2022	2038	MAP1B 9.
FT	REPEAT	2039	2055	MAP1B 10.
FT	DOMAIN	559	1035	GLU-RICH.
FT	DOMAIN	588	786	LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
FT	DOMAIN	2224	2312	LYS-RICH.
FT	CONFLICT	127	127	M -> V (IN REF. 1).
FT	CONFLICT	140	140	T -> S (IN REF. 1).
FT	CONFLICT	2112	2112	R -> K (IN REF. 3).
FT	CONFLICT	2169	2169	L -> I (IN REF. 3).
SQ	SEQUENCE	2459	AA; 269497	MW; 2E3F6872DEDB8BA2 CRC64;

Query Match 4.9%; Score 289; DB 1; Length 2459;  
 Best Local Similarity 20.9%; Pred. No. 0.00094;  
 Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

Qy 30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFFVPPA 89

Db	1004	EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDKAAEAGVTEDQY--DFL---	1058
Qy	90	PRGPLPAAPP--VAPERQPSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP	147
Db	1059	---GTPAKQPGVQSPSPREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEF	1106
Qy	148	PASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ	207
Db	1107	TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNEEETESPSQ	1150
Qy	208	E-----DFPSVLLETAASXP---SLSPLSAASFKE----HEYLGNLSTVLPTEGTLQENV	255
Db	1151	EFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEEDKF	1210
Qy	256	SEAS-----KEVSEK-----AKTLLIDRDLTE	277
Db	1211	SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPSPPIEKTPLGERSV-N	1269
Qy	278	FS-----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIVKNK-----	314
Db	1270	FSLTPNEIKASAEGEATAVSPGVTQAVVEHCASPEEKTLEVVSPSQSVTGSAGHTPY	1329
Qy	315	----DEEEKLVSNILHXQQELPTALTCLKVEDEVVSSE--KAKDSFNEKRVAVEAPMRE	368
Db	1330	QSPTDEKSSHLPTVETENAQAVP-----VSFEFTEAKDE-NER--SSISPMDE	1374
Qy	369	EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDKKCFADSL	415
Db	1375	PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSES PFEGKNGKQGFSD--	1432
Qy	416	EQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNP---AATESIATNIFLLED-	471
Db	1433	-----KESPVS-DLTSDLYQDKQEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE	1485
Qy	472	-----PTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLT	523
Db	1486	RKLGGDGSPQTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS	1542
Qy	524	VTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES-LYPAA	580
Db	1543	VSTASVATSSSFPPTTDD-VSPSLHAEVGSHPSTEVDDSLSVSVVQTPPTTFQETEMSPSK	1601
Qy	581	QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P	611
Db	1602	EECPRMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRSQSPDHP	1661
Qy	612	SAGASVIQ-----PSSSPLASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG	657
Db	1662	TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPPTTEEPSYTDNDLSELISVSQVEASP	1721
Qy	658	IKEEIKEPENINAALQETE-----APYISACDLIKE---TKLSAEP-----	696
Db	1722	STSSAHTPSQIASPLQEDTLSDVPPRDMSLYASLASEKVSLEGEKLSPKSDISPLTPR	1781
Qy	697	-----APDFS DYSEMAK-----VEQPVPDHSELVEDS-----	723

Db 1782 ESSPTYSPGFSDSTSGAKESTAAYQTSSSPPIDAAAAEPYGFRSSMLFDTMQHHLALSRD 1841  
 Qy 724 -----SPDSEPVDLFSDD---SIPDVP----QKQD 746  
 ||| | | | : || :| :  
 Db 1842 LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYEYKTE 1901  
 Qy 747 ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD 797  
 |: | |:| : | || : | ||| | : ::  
 Db 1902 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTRTPEEGGYSY-----EISEK 1953  
 Qy 798 TLLPDEVs--TLskKEIPLQMEELSTAVYSNDD-----LFISKEA 836  
 | ||| | | |: ::::| :| | :|  
 Db 1954 TTRTPEVSGYTYEKTERSRRLLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 2013  
 Qy 837 QIRETETFSdSSP-----IEIIDEFPTLISSKTDsFSKLAREYT-----DL 877  
 || | : || | :: : | | : | || ||  
 Db 2014 YSYETTTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 2073  
 Qy 878 -----EVSH-KSEIANA---PDG---AGSLPCTELPHDLsLKNIQP-----KV 913  
 | | |:|: : | : || | | | : | :  
 Db 2074 CLVSSCEFKHPKTELSPSFINPNPLEWFAGEEPTeesERPLTQSGGAPPPSGGKQQGRQC 2133  
 Qy 914 EEKISFSDDFSKNGSATSsKVLllPPDVsalGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970  
 :| | | | | ||: | || |: | | : :|:|  
 Db 2134 DETPPTSVSESAPSQTDSdV---PPETE-----ECPSITADANLDSEDESEtIPTDKT 2183  
 Qy 971 -----TEKEDRSPS-----AIFsADLGKTSVVDLLYWRDIKKTG 1004  
 :|||| | :|| | | |||  
 Db 2184 VTYKHMDPPPAPMQDRSPSPRHPDVSMVDPEALAIEQNLGKALKKDLKEKAKTKKPG 2240

Search completed: September 3, 2004, 16:06:11  
 Job time : 24.6624 secs